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L3: Entry 2 of 2

File: USPT

Jun 5, 1979

DOCUMENT-IDENTIFIER: US 4157390 A TITLE: Process for vaccine preparation

CLAIMS:

1. A process for the preparation of a <u>vaccine</u> for parenteral administraion to pregnant mammals as a means for reducing the incidence of neonatal diarrhoea, in which process K88a,b/adhesion factor of an enteropathogenic strain of E. coli is adsorbed from a cell-free aqueous solution onto erythrocytes possessing their natural surface characteristics, the ratio of adsorbed K88a,b/adhesion factor to the volume of erythrocytes present being in the range 125 to 800 hemagglutination units per ml, and the composition so formed is rendered storable by the addition thereto of a preservative such as sodium <u>azide</u> or formalin.

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Ogerigo oryza seriv

Ogewego manihot esc

Ogles9 arabidopsis

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Oglew9 suaedanonas

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Ogwego clostridium

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Ogjogo human coxsa
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Q9erm5 mus musculu
Q9y817 schizosacch
Q9y83 drosophila
G5168 salmonella
Q9f9z serratia en
Q9f9v6 human coxsa
Q917y4 pseudomonas
09aqq9 bacillus su
P77939 rhizobium s
09ev50 stappylococ
022640 raphanus sa
09sb22 oryza sativ
09rjk9 streptomyce
09zwy7 oryza sativ
09zzi9 oryza sativ
09zzi9 oryza sativ
                                                           Q9RJK9
Q9ZWH7
Q9ZWH7
Q9FEK5
Q9LDS9
Q9SW99
  Q9AQQ9
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O22640
Q9SB22
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                                                                                  Search time 41.42 Seconds (without alignments) 121.122 Million cell updates/sec
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                            hits satisfying chosen parameters:
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                                                             - protein search, using sw model
                                                                                  August 22, 2002, 07:45:22
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Q98R512
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Q92PK6
Q9SPT7
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Q940G2
Q91AS2
Q91AS2
Q91AS1
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Q91AS1
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Mizuno K., Fukuda D., Kakihara M., Kohno M., Ha T.L., Sonomoto K.; "Purification and Gene Cloning of Catalase from Staphylococcus warneri
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NOBL_TAXID=3707;
    [1]
SEQUENCE.
MEDLINE=92405676; PubMed=1526235;
Westblom T.U., Phadnis S., Langenberg W., Yoneda K., Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 505;
                                                                                                                                                                                                                             51.6%; Score 81; DB 2; Length 16; 100.0%; Pred. No. 1.6e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                             "Catalase negative mutants of Helicobacter pylori.";
Eur. J. Clin. Microbiol. Infect. Dis. 11:522-526(1992).
SEQUENCE 16 AA: 1706 MW; A3EA880275367560 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
Prodom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; UNKNOWN_1.
PROSITE; PS00438; CATALASE.2; 1.
SEQUENCE 505 AA; 58042 MW; 106AF448457EC1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALAE (EC 1.111.16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBL_TaxID=1292;
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Pred. No. 0.0021;
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58.6%;
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HSSP; P42321; 2CAE.
                                                                                                                                                                                                                             Query Match 51.6
Best Local Similarity 100.
Matches 16; Conservative
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nes 17; Conserv
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Matches 17;
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Q9ZPK6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica juncea (Leaf mustard) (Indian mustard).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicaceae; Brassica.
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01-MAY'2000 (TrEMBLrel. 13, Last sequence update)
01-MAY'2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CATALASE (FRAGNENT).
Helicobacter pylori (Campylobacter pylori).
Helicobacter:
Froteobacteria; epsilon subdivision; Helicobacter group;
NCBI_TAXID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pua E.C.;
"Molecular cloning and expression of catalase genes in Brassica
    0022254 a 0091985 H 0091985 H 00919882 H 0091982 H 0091982 H 0091988 H 0091987 H 00919
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Pred. No. 0.00035;
4; Mismatches 3; Indels
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56946 MW; EA6C455E40E045AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; AF104454; AAD17936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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InterPro; IPR002226; Catalase.
Pfam; PR00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
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01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.9%;
Best Local Similarity 66.7%;
Matches 14; Conservative
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SEQUENCE 492 AA; 56946
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eurosids II; Bra:
NCBL_TaxID=3707;
  4444444444

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Q9R512;
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                                                                                          09M4X3
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                                             RESULT
Q9M4X3
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                                                                                   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY).
-!- CATIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; AF104452; AAD17934.1;
-HSSP; P21179; 1CF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISMS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica juncea (Leaf mustard) (Indian mustard).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudlcotyledons; core eudlcots; Rosidae;
Surosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PROXIDE (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.

R EMBL: AFIOH453; ABLC.

InterPro; IPR002226; Catalase.

R PRIMTS; PR000639; catalase; 1.

R PRIMTS; PR000651; Catalase; 1.

R PRODOM; P0000510; Catalase; 1.

R PROSTIE; PS00439; Catalase; 1.

R PROSTIE; PS00438; CATALASE.

R PROSTIE; PS00438; CATALASE.
                                          *Molecular cloning and expression of catalase genes in Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and expression of catalase genes in Brassica
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Pred. No. 0.0057;
                                                                                                                                                                                                                                          InterPro; IPR00226; Catalase.
Pfam; PF00199; Catalase; 1.
Promon; PR00067; CATALASE.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 Aa; 56828 WW; 3AD5D73AF1AD7C5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.8%; Score 75; DB 10; Length 492; 61.9%; Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALASE (EC 1.111.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 13; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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09SYT7
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-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.

EMBL, AF248491; AAF71742.1; -.
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY054663; AAK9688441.
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Raphanus.
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Kwon S.-I., An C.-S.; "Characterization and expression of the catalase gene from small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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InterPro; IPR00226; Catalase.
InterPro; IPR00199; catalase. 1.

PRIMIS: PR0000510; Catalase; 1.

PROSTIE; PS00437; CATALASE. 1; 1.

PROSTIE; PS00438; CATALASE. 2; 1.

Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase. SEQUENCE 492 AA; 56817 MW; 03E38F08D038276E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                        Last sequence update)
Last annotation update)
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Pred. No. 0.0057;
492 AA
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                                                            Created)
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   PRT;
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61.98;
                                                      01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                        Raphanus sativus (Radish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.8
Best Local Similarity 61.9
Matches 13; Conservative
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   PRELIMINARY;
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Gaps

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Indels

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Sanz R., De la Fuente R.;
"Catalase deficiency in Staphylococcus aureus subsp. anaerobius is associated with natural loss of function mutations within the structural gene.";
Microbiology 146.465-475(2000).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                           47.1%; Score 74; DB 10; Length 41; 66.7%; Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 2; Length 455;
Pred. No. 0.0074;
2; Mismatches 11; Indels
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SEQUENCE 455 AA; 52618 MW; E29A5B259D642CAC CRC64;
                 Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. BMBL; Y10785; CAR717571; -.
Interpro; IRN002226; Catalase.
Pfam; PF00199; catalase; 1.
Hypothetical protein.
NON_TER 41 A1, 4499 WW; 51046FE68DFD2EDI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEROXIDE (BY SIMILARITY).
-!-CATALIYICA GCTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
EMBL; AJ000471; CAB76840.1; -
HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
Bacteria: Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                   455 AA.
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                                                                                                                                                                                         1; Mismatches
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Thesis (1998), UNIV COMPLUTENSE MADRID.
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                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=20170679; Pubmed=10708385;
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Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                        9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                     18 TTNAGAPVWKDIEVMTVGPRG 38
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55.2%;
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                                                                                                                                                         Query Match 47.1'
Best Local Similarity 66.7'
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             CATALASE (EC 1.11.1.6).
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        stapfianus.";
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Q9RG14
ID Q9RG14
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Q9L4S2
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHERICAL 4.5 KDA PROTEIN (FRAMBRN).
Sporobolus stapfianus (Ressurection grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; Poaceae; Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                                                                                                                                                                  Brassica juncea (Leaf mustard) (Indian mustard).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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Blomstedt C.K., Gianello R.D., Neale A.D., Hamill J.D., Gaff D.F.;
"Isolation and characterization of cDNAs associated with the onset of desiccation tolerance in the resurrection grass Sporobolus
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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   Similarity 61.9%; Score 75; DB 10; Length 492; Similarity 61.9%; Pred. No. 0.0057; 13; Conservative 4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 496 AA; 57411 MW; 23DAA98786DC4E5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALARE (EC 1.111.16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4:
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                                                                                                                                                                           496 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; P0000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG 29
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                                                                TTAFGAPVWDDNNVITAGPRG
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Best Local Similarity 61.9°
Matches 13; Conservative
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3707;
Query Match
Best Local Simi
Matches 13;
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Q9ZPK7;
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Lancet 357:1225-1240(2001).

-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY).
-!- CATIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.
EMBL; AP003133; BAB474771; -.
EMBL; AP003362; BAB57496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECIES-S.aureus (strain N315), and S.aureus (strain Mu50);
SPECIES-S.aureus (strain N315), and S.aureus (strain Mu50);
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."
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  HYDROGEN
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                                                            EMBL; AJ000472. CAB76839.1; -...
EMBL; AJ000472. CAB76839.1; -...
HASP; P42311; 2CAE.
InterPro; IPR002225.
EMBL; AF00199; catalase.
Propom; PRO0057; CATALASE.
PROSTIE; PS00433; CATALASE.1.
PROSTIE; PS00438; CATALASE.1.
Heme; Hydrogen peroxidase.
SEQUENCE 508 AA; S8324 MW; BEEB05FBB0AE172F CRC64;
                                                                                                                                                                                                                                                                                                                                         Ouery Match
47.1%; Score 74; DB 2; Length 505;
Best Local Similarity 55.2%; Pred. No. 0.0083;
Matches 16; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
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  CELLS FROM THE TOXIC EFFECTS OF
                                         2 H(2)O(2) = O(2) + 2 H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain Mu50).
Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
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PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSTIE; PS00437; CATALASE.; 1.
PROSTIE; PS00438; CATALASE.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002226; Catalase.
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55.28;
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KATA OR SA1170 OR SAV1334.
                PEROXIDE (BY SIMILARITY
-!- CATALYTIC ACTIVITY: 2 H
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Best Local Similarity 55.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
  TO PROTECT
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SEQUENCE
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Q99UE2
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Figurski D.H.;
Direct Selection of IS903 Transposon Insertions by Use of a Broad-Host-Range Vector: Isolation of Catalase-Deficient Mutants of Actinobacillus actinomycetemcomitans.";
J. Bacteriol. 181:729997307(1999).
J. PONCTION: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
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Microbiology 146:465-475(2000).
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                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Actinobacillus.
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SEQUENCE 484 AA; 54961 MW; D0E523AB2557DBCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEROXIDE (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.
EMBL; AF162654; AAF17882.1; -.
                   01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE (EC 1.111.16).
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Last annotation update)
                                                                                                                                       Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
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Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hesis (1998), UNIV. COMPLUTENSE MADRID.
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STAILN-ATCC 12600;
MEDLINE-20170679; Pubmed-10708385;
Sanz R., De la Fuente R.;
                                                                                                                                                                                                                                                                                                  STRAIN-Y4NAL;
MEDLINE-20042351; PubMed-10572134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P42321; 2CAE.
InterPro; 1PR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00065; CATALASE.
PRODOM; P0000510; CATALASE.
PROSITE; PS00437; CATALASE 1:
PROSITE; PS00438; CATALASE 1: 1.
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66.78;
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Best Local Similarity 66.7;
Matches 14; Conservative
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                                                                                                                                                               actinomycetemcomitans)
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SEQUENCE FROM N.A.
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STRAIN-ATCC 12600;
Sanz R.;
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                                                                                                                                                                                                                                 NCBI_TaxID=714;
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09L4S1;
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InterPro; IPR002226; Catalase.
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Q9AQQ9;
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                                                                                                                                                                                                                                                      TISSUE-LEAF;
Lino-Neto T., Tavares R.M., Palme K., Pais M.S.S.;
Lino-Neto T., Tavares R.M., Palme K., Pais M.S.S.;
Lino-Neto T., Tavares during senescence and regreening of
Zantedeschia aethiopica spathe.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS. FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thome H., Happe T.;
Submitted (MAY-11997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                Zantedeschia aethiopica (White calla lily).
Sukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Zantedeschia.
NCBL_maxID=69721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56968 MW; DC9F3EB1392DEICF CRC64;
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-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; V13220; CATA3663.1; -.
HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                        PEROXIDE (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.
                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALAEE (EC 1.111.1.6).
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Last annotation update)
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           29
                        Created)
          MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                               PRT;
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Therpro; IPR002256; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
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61.9%;
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                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF207906; AAF19965.1;
HSSP; P21179; 1QF7.
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                                                                                              PRELIMINARY;
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Best Local Similarity
Matches 13; Conserv
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009484
ID 009484
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SETALINE-CC-125 WILD TYPE MT+ 137C;
Kim J.Y., Park K.Y., Lee K.O., Lee S.H.;
IISOlation and characterization of a cDNA encoding a catalase from Chlamydomonas reinhardtii (Accession No. AF016902) (PGR 00-016).";
Plant Physiol. 122:293-293(2000).
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                   Length 492;
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PRINTS; PR00169; CATALASE.
PRODOM; P0000510; CATALASE.; 1.
PROSITE; PS00438; CATALASE.; 1.
PROSITE; PS00438; CATALASE.; 1.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 493 AA; 55943 MW; 2874B2BBACCEE773 CRC64;
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
Probom; PD000510; Catalase; 1.
PROSITE; PS00438; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56227 MW; 3711B90126911C32 CRC64;
                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 \text{ H}(2)0(2) = 0(2) + 2 \text{ H}(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                 Score 72; DB 10;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                         493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483 AA.
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                            3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                      9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEROXIDE (BY SIMILARITY).
                                                                                                                                                                                                 Query Match
Best Local Similarity 61.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             022472;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                               Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3055;
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1D 099

AC 099

DT 011

DT 011

DE CA
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SEQUENCE FROM N.A.

11 K.-S., An C.-S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raphanus sativus (Radish).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINSCURED STRAIN C2A;
STRAINSCURED STRAIN C2A;
Barriere C., Brueckner R., Talon R.;
"Characterization of catalases in Staphylococcus xylosus.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ259151; CAR.
ESSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%; Score 71; DB 2; Length 493; 65.2%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56874 MW; 900B959518A9404B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 H(2)0(2) - 0(2) + 2 H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                   Staphylococcus xylosus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 AA
                                                                                                                                   493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
Oxidoreductase; Peroxidase.
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                    7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KLTGLFGAPVSDRENSMTAGPRG 26
  7 KQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, CATALASE (EC 1.11.1.6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.2
Matches 15; Conservative
                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            022640;
                                                                                                                                                        Q9EV50;
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                                                                                                                                   Q9EV50
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022640
                                                                                                 13
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                                                                                                                 Q9EV50
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                                                                                       Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                         Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 483 AA; 54756 MW; 1D423F71AC8CDDBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iron; Heme; Hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEROXIDE.

-1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.

-1- COFACTOR: HEME GROUP.

EMBL: U56239; AAA9823.1; -.

HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 45.2%; Score 71; DB 2; Best Local Similarity 60.9%; Pred. No. 0.023; Matches 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.2%; Score 71; DB 2;
ilarity 65.2%; Pred. No. 0.023;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                 Interpro; IPR00226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro: IPR00226; Catalase.
Pfam: PF00199; Catalase; 1.
PRINTS: PR006067; CATALASE.
PROSITE: PS00437; CATALASE.1; 1.
PROSITE: PS00438; CATALASE.1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ||::|||| |: |||| || 5 KLTTSWGAPVGDNQNSMTAGSRG 27
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Rhizob'''
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Peroxidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Bacillus subtilis
                                                      NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kwon S., An C.;
Submitted (AUG-1
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P77939;
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NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                              Theor. Appl. Genet. 97:9-19(1998).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Bukaryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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                                                        DB 10; Length 491;
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           Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 491 AA; 56716 MW; 7C20151C3BB16664 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heme, Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56575 MW; 8C49D4FE45993FC8 CRC64;
                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; D64013; DAA34204.1; -.
HSSP; P21179; 10F7.
                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE (EC 1.111.1.6).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                      Query Match 44.6%; Score 70; DB 10 Best Local Similarity 60.0%; Pred. No. 0.033; Matches 12; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.6%; Score 70; DB 10; 57.1%; Pred. No. 0.033; ive 4; Mismatches
                                                                                                                                                                                 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00067; CATALASE.
PRODOIT: PR00015; CATALASE.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
PROSITE; PS00438; CATALASE_2; 1.
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Pfam; PF00199; catalase; 1.
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18 TNSGAPVWNNNSSMTVGPRG 37
                                                                                                    10 TAFGAPVWDDNNVITAGPRG 29
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.6
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                           TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09RJK9;
                                                                                                                                                                                 Q9SB22
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                                                                                                                                                           RESULT 21
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Gaps
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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"Cloning and expression of a new rice catalase gene.";

"Cloning and expression of a new rice catalase gene.";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO20502; BA34714.1; -..

HSSP; P00432; 4BLC.

Interpro; IPR002226; Catalase.

Pfam; PF00199; Catalase; 2.

PF6m; PF00199; Catalase.

PF00m; PD000510; Catalase.

PF00m; PD000510; Catalase.

PROSITE; PS00438; CATALASE.2; 1.

SEQUENCE 492 AA; 56175 MW; ABD3D10D309443F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB 2; Length 487;
Pred. No. 0.046;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 487 AA; 55116 MW; 9D3334889EAF60B7 CRC64;
                                                                                                                                                           Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                     STRAIN=A3(2);
Murphy L., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 43.9%;
Best Local Similarity 51.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
SEQUENCE FROM N.A.
                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                   STRAIN=A3(2);
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01-DEC-2001
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Iwamoto M., Maekawa M., Saito A., Higo H., Higo K.;
"Evolutionary relationship of plant catalase genes inferred from exon-
intron structures: isozyme divergence after the separation of monocots
and dicots.";
Theor. Appl. Genet. 97:9-19(1998).
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Hevea.
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                DB 10; Length 492;
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Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ide; Iron; Oxidoreductase; Peroxidase.
56806 MW; B14CE64C275213C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; D66611; BAA34205.1; -.
HSSP: P00432; 4BLC.
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Last annotation update)
                                                    5.
                                0.046;
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                                                      Mismatches
                Score 69;
Pred. No.
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                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                        9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                            9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.9%;
            43.9%;
ilarity 57.1%;
Conservative 4
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                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19,
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
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Best Local Similarity 57.1%
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SEQUENCE 492 AA; 56806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
                                Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-4530;
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01-MAR-2001
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                Query Match
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Q9ZRI9;
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SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lerz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56705 MW; 73C4361F837EEB8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0c1-2000 (TrEMBLrel. 15, Created)
01-0c1-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALAEE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 10;
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1013 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                              Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                     InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.3%;
Best Local Similarity 57.1%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 TINSGAPVWNNNSSLTVGARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Submitted (APR-2000)
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Ichise N., Morita N., Hoshino T., Kawasaki K., Yumoto I., Okuyama H.; "Cloning of the Complete Catalase Gene from the Hydrogenperoxide-
                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Suaeda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=76258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistant Bacterium Vibrio rumoiensis S-1 and Its Subcelluar localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.7%; Score 67; DB 10; Length 492; Best Local Similarity 57.1%; Pred. No. 0.093; Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Wang P.P., Ma C.L., Sun Y.F., Zhao Y.X., Zhang H.;
Wang P.P., Ma C.L., Sun Y.F., Zhao Y.X., Zhang H.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF390210; AAK67359.1;
SEQUENCE 492 Aa, 56788 MW; 8532135DE66DA3B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB030821; BAB12412.1; -.
HSSP; P42321; 2CBE.
InterPro; IRR002226; Catalase.
PRINTS; PR00199; catalase; 1.
ProDon; PD000510; Catalase; 1.
ProDon; PD000510; Catalase; 1.
PROSITE; PS000437; CATALASE.1; UNKNOWN_1.
SEQUENCE 509 AA; 57659 MW; CE3A2B4FDIC7DEE8 CRC64;
                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last sequence update)
Last annotation update)
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61.9%; Pred. No. 0.14;
Live 3; Mismatches
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                                                                                                                                                                                                                                                                                 Suaeda maritima subsp. salsa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9FAZ3;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE VKTA.
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                                                                                                              PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S-1;
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                                                                                                                                                                                                                                      CATALASE.
                                                                                                           094EV9
                                                                                                                                  094EV9
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
A Thaveri A., Toriuni M., Vaysberg M., Yu G., Davis R., Federspiel N.,
A Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
PEROXIDE (BY SIMILARITY).
--- CATALITY: 2 H(2)0(2) - O(2) + 2 H(2)0.
REMBL, ACC06251; AAF796251; --
REMBL, ACC062551; AAF796251; --
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TISSUE-STORAGE ROOT;
MEDLINE-21210978; PubMed-11311947;
Reilly K., Han Y., Tohme J., Beeching J.R.;
"Isolation and characterisation of a cassava catalase expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MEC-2001 (TrEMBLrel. 19, Last annotation update)
CAPALASE CAT1 (EC 1.11.1.6).
Manihot esculenta (Cassava) (Manioc).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Manihot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.3%; Score 68; DB 10; Length 1013; 57.1%; Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Peroxidase.; 604797360DB8486D CRC64;
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Blochim. Blochs Acta 1518:317-323(2001).
EMBL; AFT70272; AAD50974.1; -.
HSSP; P21179; 1CF9.
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InterPro; 1PR00226; Catalase.
Ffam; PP00199; Catalase; 2.
PRINTS; PR00067; CATALASE.
PRODOM; P0000510; Catalase; 2.
PROSITE; PS000437; CATALASE.1; 2.
PROSITE; PS00438; CATALASE.2; 1.
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116681 MW;
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Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
Oxidoreductase; Peroxidase.
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Best Local Similarity 57.18
Matches 12; Conservative
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Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heme; Hydrogen peroxide; SEQUENCE 1013 AA; 116
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509 AA

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Length 509; Indels us-09-488-737-2.rspt

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                                                                                                                                                                                                                                                             493 AA.
                    41.4%; Score 65; DB 61.9%; Pred. No. 0.2; ive 2; Mismatches
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Neisseria meningitidis (serogroup B).
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STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761119;
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                                                                                                          9 TTAFGAPVWDDNNVITAGPRG
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KATA OR NMA0050 OR NMB0216.
                                                               13; Conservative
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Best Local Similarity
                                    Best_Local Similarity
Matches 13; Conserv
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                        Query Match
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081337
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Q9JRF5
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MEDLINE-20579473; PubMed-11137458;

MEDLINE-20579473; PubMed-11137458;

Makamura K., Watanabe M., Takanaka K., Sasaki Y., Ikeda T.;

"CDNA cloning of mutant catalase in acatalasemic beagle dog: single in nucleotide substitution leading to thermal-instability and enhanced proteolysis of mutant enzyme.";

Int. J. Blochem. Cell Biol. 32:1183-1193(2000).

R EMBL; AB038231; BAB20764.1; -.

R HSSP; PR0005225; Catalase.

R InterPro: IPR002225; Catalase.

R Propom; PR000510; Catalase; 1.

R PROSTTE; PS0006510; Catalase: 1.

R PROSTTE; PS00437; CATALASE.

R PROSTTE; PS00437; CATALASE.
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Canis familiaris (Dog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PROSTOR; PS00437; CATALASE.
PROSTIE; PS00437; CATALASE.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 527 AA; 59733 MW; 637A97F24FFIE15A CRC64;
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                                                               Last sequence update)
Last annotation update)
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Last annotation update)
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0.14;
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Pred. No. 0.14;
0; Mismatches
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527 AA
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PRT;
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                                      01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-DEC-2001 (TrEMBLrel, 19, CATALASE (EC 1.11.1.6).
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Best Local Similarity 66.73
Matches 14; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                NCBI_TaxID=9606;
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                      09BWT9;
Q9BWT9
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Q9GKY3
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Transcription of catalase are expressed in leaves and roots of the common ice plant.";
The common ice plant.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
HSSP: P21179; 1CF9.
R HSSP: P21179; 1CF9.
R HSSP: P21179; 1CF9.
R PRINTS; PR000226; Catalase.
R PRINTS; PR00067; Catalase.
R PROSITE: PS000437; CATALASE.
R PROSITE; PS000437; CATALASE.
R PROSITE; PS000437; CATALASE.
W Oxidoreductase; Peroxidase.
Oxidoreductase; Peroxidase.
Oxidoreductase; Peroxidase.
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NCBI_TaxID=65699, 491;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ROOT CATALASE (EC 1.11.1.6).
Mesembryanthemum crystallinum (Common ice plant).
Mesembryanthemum crystallinum (Common ice plant).
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyliidae, Caryophyliales; Alzoaceae; Mesembryanthemum.
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Length 527;
                                                                     Indels
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Last sequence update)
Last annotation update)
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Peters M., Heinaru A., Nurk A.;
Plasmid-encoded catalase KatA, the main catalase of Pseudomonas
fluorescens strain CD56.";
FEMS Microbiol. Lett. 200:235-240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                         Query Match 40.8%; Score 64; DB 13; Length 526; Best Local Similarity 57.1%; Pred. No. 0.29; Matches 12; Conservative 2; Mismatches 7; Indels
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Heme; Hydrogen peroxide; Tron; Oxidoreductase; Peroxidase.
SEQUENCE 526 AA; S9542 MW; 9FA05042737662A4 CRC64;
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Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Pfam; PF00199; Catalase; 1.
PRINTS; PR000067; CATALASE.
PRODOM; PD000510; CATALASE.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                               28 TTGAGVPIGDKLNAMTAGPRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TTAFGAPVWDDNNVITAGPRG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U72068; AAB17009.1; -- HSSP; P42321; 2CAE.
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01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas fluorescens.
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SEQUENCE FROM N.A.
STRAIN=PM70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pAM10.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=294;
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NCBI_TaxID=747;
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SEQUENCE
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P77924;
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Q9CPK5
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                                                                                                                                                                   AEDINAMOS SERGROUP B;
MEDLINE=2017575; PubMed=10710307;
MEDLINE=2017575; PubMed=10710307;
MEDLINE=2017575; PubMed=10710307;
MEDLINE=2017575; PubMed=10710307;
Bisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Felischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PROXIDE (EW SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.
EMBL; AF170069; AAF89686.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Grundy M.A.; Gerundy M.A.; Gerundy M.A.; Mard G.S., Kauffman B.J., Grundy M.A.; Moblecular cloning and sequence analysis of the Danio rerio catalase gene.";
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 64; DB 16; Length 504; Pred. No. 0.27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Peroxidase; Complete proteome.
SEQUENCE 504 AA; 57167 MW; 26858B47446F3775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALASE (EC 1.11.1.6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comp. Biochem. Physiol. 127:447-457(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510, Catalase; 1.
PROSITE; PS00437; CATALASE_1; UNKNOWN_1.
PROSITE; PS00438; CATALASE_2; 1.
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EMBL; AL162752; CAB83367.1; -.
EMBL; AE002379; AAF40672.1; -.
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InterPro; IPR002256; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE:
ProDom; PD000510; Catalase; 1.
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16 GAPVADNQNSLTAGPRG 32
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Best Local Similarity 70.6
***ches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 GAPVWDDNNVITAGPRG 29
                                                           meningitidis Z2491.";
Nature 404:502-506(2000).
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                                                                                                                                                   SEQUENCE FROM N.A.
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Helianthus
Heliantheae; He
NCBI_TaxID=4232
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081336
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                                                                                                                                                                                 Gaps
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       May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006036; AAK02116.1;
                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helianthus annuus (Common sunflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
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                                                                                                                                                           38.9%; Score 61; DB 16; Length 484; 47.6%; Pred. No. 0.74;
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Pred. No. 0.73;
                                                                                                                                                                                 4; Indels
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                                                          PICTOR TRO02226; Catalase.
PRINTS; PR00199; Catalase; 1.
PRINTS; PR00057; CATALASE.
PRODOM; PD000510; CATALASE.
PROSITE; PS00437; CATALASE_1; 1.
COMPLEE POTCEOME.
SEQUENCE 484 AA; 55127 MW; 5BE648D3610A6420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 349 Aa; 37380 MW; 4A71A677ECE3D3A4 CRC64;
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Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE (EC 1.11.1.6).
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                                                                                                                                                                                                                                                                                349 AA
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                                                                                                                                                                               7; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-CT-2001 (TrEMBLrel. 18, Last anno
UNKNOWN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                PRT;
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MEDLINE-21235186; PubMed-11337471;
MEDLINE-21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 KWTTTFGAKESIWDDTNVIGVTP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 KQTTAFGA--PVWDDNNVITAGP 27
                                                                                                                                                                                                    9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                  38.2%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006267; AAK04397.1;
                                                                                                                                                                    Best Local Similarity 47.6 Matches 10; Conservative
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                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                  HSSP; P42321; 2CAE.
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                                                                                                                                                                                                                                                                                                                                                                            Lactococcus
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Best Local S:
Matches 13;
                                                                                                                                                            Query Match
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Q9M504;
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Q9CIQ7
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CV. SPANNERS ALLZWECK; TISSUE=COTYLEDONS;

Heinze M., Baur B., Eising R.;

Heinze M., Baur B., Eising R.;

Biogenesis of catalase forming the crystalline inclusions in peroxisomes of sunflower cotyledons ";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN SERVES TO AREALY TOXIC EMBL; AF243517; AAF61732.1; -...

EMBL; AF243517; AAF61732.1; -...

RMSP; PORO433, HBLC.

EMBL; AF243517; CATALASE.

PROSTIE; PRO00510; Catalase; 1.

PRINTS; PRO00510; Catalase; 1.

PROSTIE; PSO0433; CATALASE.

PROSTIE; PROSTIE; PROMETER CATALASE.

PROSTIE; PROSTIE; PROMETER CATALASE.
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Michalowski C.B., Quigley-Landreau F., Bohnert H.J.;
Michalowski C.B., Quigley-Landreau F., Bohnert H.J.;
The common ice plant.;
The common ice plant.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
C. Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
C. I- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SRRVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
C. PEROXIDE (BY SIMILARITY).
C.I- CATALYTIC ACTIVITY: 2 H(2)0(2) - O(2) + 2 H(2)0.
EMBL; AF065319; AAC19397.1; -.
DR RISSP; P21179; ICF9.
BR InterPro: IPRO01256; Catalase.
DR PROMOFO; CATALASE.
PRODOM: PD000510; Catalase.
DR PROSITE; PS00437; CATALASE.
DR PROSITE; PS00438; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum. NCBI_TaxID=3544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56931 MW; AADF2B516C130163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56886 MW; 6DD5DBOAFAAD5C60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE (EC 1.111.1.6).
Mesembryanthemum crystallinum (Common ice plant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ς.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  492 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.6%;
Best Local Similarity 52.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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RC TRAIN=ATCC10147;

RX MEDLINE=97334128; PubMed=9190825;

RX Gho Y.H., Roo J.H.;

RD choil T.H., Roo J.H.;

RY CAD 3.H.;

RY Vegetative catalase in Streptomyces coelicolor muller.";

LY SECTION TO CCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

FROMELY SPEROXIDE (BY STRITAY).

C -1 - CATALITIE CATALIASE.

DR FROM PROSITE; PSO0037; CATALIASE:

DR PROSITE; PSO00437; CATALIASE:

DR PROSITE; PSO0439; CATALIASE:

NR PROSITE; PSO0439; CATALIASE:

NR PROSITE; PSO0439; CATALIASE:

NR PROSITE; PSO0439; CATALIASE:

NR PROSITE; PSO0439; CATALIASE:

SEQUENCE 488 AA; 55440 MW; 323633B73E46C7C8 CRC64;
                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBL_TaxID-1902;
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                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE (EC 1.11.1.6).
                                                                                                                                                        488 AA.
                                                                                                                                                        PRT;
9 TTAFGAPVWDDNNVITAGPRG 29
                         || || ||||:::|: :| || || || TINSGAPVYNNNSSLIVGIRG 38
                                                                                                                                                        PRELIMINARY;
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SEQUENCE FROM N.A.
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P77948;
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                                                                                                            RESULT
P77948
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Search completed: August 22, 2002, 07:45:26 Job time: 145 sec

3 NKDVKQTTAFGAPVWDDNNVITAGPR 28

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Gaps

Run

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097pv3 streptococc 09f9s8 edta-degrad 09rg53 streptovert 093t39 streptomyce 09x638 leptospira 09x691 coxiella bu 092596 rhizobium m 092596 ryza sativ 09raj9 moraxella s
                                                           099w61 staphylococ
099iy68 prototheca
09c2p1 neurospora
040450 nicotiana s
09axu2 pelargonium
093y56 arabilopsis
043364 nicotiana s
095tv3 drosophila
09687 drosophila
09687 drosophila
09681 theileria a
09819 xylella fas
09196 candidatus
02614 toxoplasma
09tm9 toxoplasma
09tm9 toxoplasma
                                                                                                                                                092191 arabidopsis
099206 arabidopsis
091026 caen mays (m
019072 caenorhabdi
09891 mycoplasma
033451 eimeria ten
025820 plasmodium
0994m7 drosophila
095513 loofah witc
09791 thermoplasm
095633 methanoccocc
                                                                                                                                                                                                                       Q91n13 arabidopsis
Q42336 arabidopsis
O49736 arabidopsis
Q9K713 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                               Q9hpe4 halobacteri
045622 caenorhabdi
09trq9 sus scrofa
09n9d5 scoliopteri
Q9naO7 drosophila
064490 arabidopsis
Q9zv47 arabidopsis
                                                  Q9cei0 lactococcus
Q9tlv8 cyanidium c
                                                                                                                                                                                                                   Q978w8 thermoplasm
                                                                                                                               Q26114
Q9TMM9
O78325
Q9ZT91
Q39206
Q9FUZ6
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Q42336
Q42336
Q49736
Q9K7L3
Q9HPE4
                                                                                                                                                                                                                                                                                                                                                                                          Q9TRQ9
Q9N9D5
Q9NA07
O64490
Q9ZV47
Q97PV3
Q9F9S8
Q9RG53
Q93T39
Q9XD38
Q9XG1
Q9X61
Q9X61
Q9SEF8
                                                  Q9CEI0
Q9TLV8
Q99W61
                                                                  Q9TJQ8
Q9C2P1
Q40450
Q9AXU2
Q93Y56
Q43364
Q95TV3
Q9V6Q7
Q78381
Q9P9Q9
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P91150
Q976B1
Q25099
029514
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P93769
Q9C5L4
Q39093
Q9ASU9
Q94AD0
                                                                                                                                                                  Q19072
Q98QG1
Q33451
Q25820
Q9V4M7
Q9S513
Q979T1
Q93638
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P94009
P94008
P94007
                                                                                                                                                                                                                         Q980A5
Q975N8
                                                                                                                                                                                                                                                                                082788
                                                                                                                                                                                                                                    Q9HNK9
                 Q9kv37 vibrio chol
Q9kuzó vibrio chol
Q9Z16 listeria in
Q9K117 neisseria m
Q9T15 neisseria m
Q9T42 porphyromon
Q9Th11 porphyromon
Q9Th10 porphyromon
Q9Th10 porphyromon
Q9Th10 borphyromon
Q9Th10 borphyromon
Q9Th10 borphyromon
                                                                                                                                                                                                                                                                                                                                                                                           Q999m0 caulobacter
Q933r9 ureaplasma
Q929w4 rickettsia
Q94755 streptomyce
Q9hwd3 pseudomonas
                                                                                                                                                                                                                                                                                                                              Q97eh5 clostridium
                                     2002, 07:43:01; Search time 41.42 Seconds (without alignments) 91.885 Million cell updates/sec
                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                   Description
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                               hits satisfying chosen parameters:
                                                                                                    562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                       summaries

    protein search, using sw model

                                                                        1 MKEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                        09KUZ6
092716
092717
09417
097815
097815
0978110
0978110
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Q9RG55
Q9HWD3
                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                   sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                      sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                           sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                     sp_rvirus:*
sp_bacteriap:*
                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 100
                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                                                                       sp_archea:*
sp_bacteria:*
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16
16
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10
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                                                             US-09-488-737-1
                                                                                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                  SPIREMBL_19:*
                                                                                                                                                                                                                                                                                                                   Length
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Match
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990.23
990.23
997.00
987.00
987.00
986.23
986.23
                                                                                                                                           Post-processing:
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                                                             Title:
Perfect score:
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1111
1109
1107
1107
1107
1106
1106
1106
                                                                                    Scoring table:
                                                                                                                           Minimum DB
Maximum DB
                             OM protein
                                                                          Sequence:
                                                                                                     Searched:
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                                        :
0
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SEQUENCE FROM N.A.
STRAINEL TOW NIG661 / SEROTYPE 01;
MEDLINE=L TOW NIG661 / DEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINEL TOW NIG661 / SEROTYPE 01;
MEDLINE-EL TOW NIG661 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Hodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AE004124; AAF93535.1; -.
                                                                                                                                                                                                                           TO THE GTP-BINDING ELONGATION FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                               'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                             43185 MW; A047E398A84B8A40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF0DE31A00618B36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      90.2%; Score 111; DB 16; 90.5%; Pred. No. 8.5e-10; iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                            Interpro; IPR00195; GTP_EFTU.
PRINTS; PR00315; ELONGATNFCT.
PROSTEE, PS00301. EFACTOR_GTP; 1.
Complete proteome; GTP-binding.
SEQUENCE 394 AA; 43185 MW; A04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00315; ELONGATNFCT.
PROSITE, PS00301; EFACTOR_GTP: 1.
COMPLETE PROFEDEN: GTP-binding.
SEQUENCE 394 AA; 43126 MW; BF(
                                                                                                                                                                                                          Nature 406:477-483(2000).
-!- SIMILARITY: BELONGS TO THE
EMBL; AE004120; AAF93494.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000795; GTP_EFTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KEKFERTKPHVNVGTIGHVDH 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                      HSSP; P02990; LETU.
TIGR; VC0321; -.
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TIGR; VC0362; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=666;
                                                                                                                                                                                                 cholerae
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Q9KUZ6
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Q9nar5 clytus arie
Q9n6t8 scoliopteri
Q9n6u3 clytus arie
Q9vfa6 drosophila
Q9n6u1 drosophila
Q9n6u1 drosophila
Q9n6u2 coliopteri
Q9n6u2 clytus arie
Q9n6u0 leptinotars
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A SEQUENCE FROM N.A.

RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

RX MEDLINE-21393925; PubMed=11466286;

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA Tatsov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Tatsov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Datesou M. Koonin B.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

RT Genome cactobutylicum.";

J. Bacteriud. 183:4833-4838(2001).

RE EMBL; AE007809; AAK81075.1;

DR InterPro: IPR004161; GTP_EFFU.

DR InterPro: IPR004161; GTP_EFFU.

DR InterPro: IPR004160; GTP_EFFU.D3.
                  leptinotars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Gacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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0
                 09n9w0
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Complete protecome.
SEQUENCE 397 AA; 43452 MW; F031B2F700434452 CRC64;
                                                                                                                                                                                                                                                                                                (TremBirel. 18, Created)
(TremBirel. 18, Last sequence update)
(TremBirel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA.
                                                                                                                                                                                              ALIGNMENTS
               0900900
090791
0900485
090618
090603
090786
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                                                                                                                    Q9N6T9
Q9N6U2
Q9N6U0
                                                                                                                                                                                                                                                                       PRT;
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Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNFCT.
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                                                                                                                                                                                                                                                                                                                                           ELONGATION FACTOR TU (EF-TU).
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                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
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 NCBI_TaxID=1488;
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01-OCT-2001 (
01-DEC-2001 (
   Query Match
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Q97ЕН5;
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Q97EH5
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09KV37
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Length 394;

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Length 394;

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P02990; 1EFU
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Q9JRI5
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STRAIN=MC58 / SEROGROUP B;
MEDLINE=201755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Charabotty T.,
Charabit A., Chetounani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Sinces N., Tierrez A.,
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelsseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                        Gaps
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                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 AA; 43353 MW; CEOFA4906D644C24 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.6%; Score 109; DB 16; 90.5%; Pred. No. 1.8e-09; iive 2; Mismatches 0;
  Pred. No. 8.5e-10;
                                                                                                                                                                                                  395 AA.
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                      Mismatches
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STRAIN-CLIP 11262 / SEROVAR 6A;
PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 294:849-852(2001).
EMBL; AL596173; CAC98028.1; -.
ListiList; LIN02802; -.
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                                                                              90.5%;
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                                                         2 KEKFNRTKPHVNIGTIGHVDH
                    Conservative
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                                                                                                                                                                                                  PRELIMINARY;
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Best Local Similarity
Matches 19; Conserv
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          Listeria innocua
                                                                                                                                                                                                                                                                                                                      FUFA OR LIN2802.
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                                                                                                                                                                                                                                                                                                   TUFA PROTEIN
                      19;
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Q9K117;
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                    Matches
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Q92716
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SERGATE FROM N.A.
STRAIN=MCS6 / SEROGROUP B;
STRAIN=MCS6 / SEROGROUP B;
MEDLINE=2017555; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Matte D.H., Salzberg S.L., White O., Fleischmann K.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Scallato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (serogroup A), and
Neisseria meningitidis (serogroup B).
Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699, 491;
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                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. EMBL, AE002372; AAF40598.1; -. HSSP; P02990; 1ETU.
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MEDLINE-2022556; Pubmed-10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 107; DB 16; Length 394; 85.7%; Pred. No. 3.8e-09;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
ELONGATION FACTOR TU (TRANSLATION ELONGATION FACTOR TU).
(TUPAL OR NMA0134 OR NMB0124) AND (TUFAZ OR NMA0149).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00315; ELONGATNFCT.
PROSTITE; PS00301; EFACTOR_GTP; 1.
Complete proteome; Elongation factor; GTP-binding, SEQUENCE 394 AA; 42925 MW; 55762F03EC048563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KEKFERSKPHVNVGTIGHVDH 23
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                                                                                                                                                                                                                                          Science 287:1809-1815(2000).
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Best Local Similarity 85.7
Matches 18; Conservative
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Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, CFB group; Bacteroidetes; Bacteroidales; Porphyromonas.
Porphyromonas.
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Nagai A., Itoh N.

Ragai A., Itoh N.

"EF-Tu sequence of Porphyromonas gingivalis.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

REMBL; AB053463; BAA88136.1; -.

RISP; PO2990; IEFU.

RICEPPO; IPR000795; GTP_EFTU.D2.

RICEPPO; IPR004160; GTP_EFTU.D3.

RICEPPO; IPR004160; GTP_EFTU.D3.

Reptam; PF031144; GTP_EFTU.D3.

Reptam; PF031144; GTP_EFTU.D3.

Reptam; PF031145; GTP_EFTU.D3.

Reptam; PF031145; GTP_EFTU.D3:

Reptam; PF03115; ELONGAINFCT.
                                                          STRAIN-FDC 381;
A Nagai A., Itoh N.;
A nagai A., Itoh N.;
Ber Tu sequence of Porphyromonas gingivalis.";
Est usequence of Porphyromonas gingivalis.
Est usequence of Porphyromonas gingivalis.

Interpro: IPR004161; GTP_EFTU_D3.

Interpro: IPR004161; GTP_EFTU_D3.

Refam: PF001444; GTP_EFTU_D2; 1.

Refam: PF001443; GTP_EFTU_D3; 1.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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85.7%; Pred. No. 3.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
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PROSITE; PS00301; EFACTOR_GTP; 1.
GTP-binding.
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Best Local Similarity 85.7%
Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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                              SEQUENCE FROM N.A.
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Q9RHI1
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Q9RHI0
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Bacteria, CFB group, Bacteroidetes; Bacteroidales; Porphyromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
                                                                                                                                                                                                                                                                                                                               Gaps
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87.0%; Score 107; DB 16; Length 394;
Best Local Similarity 85.7%; Pred. No. 3.8e-09;
Matches 18; Conservative 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.0%; Score 107; DB 2; Length 395;
85.7%; Pred. No. 3.8e-09;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-A7A1 28, AND W83;
Magai A., Itoh N.;
Magai A., Itoh N.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EEMBL; A80036464; BAA88137.1; -.
EEMBL; A80036462; BAA88135.1; -.
HSSP; P02990; 1EFU.
                 TIGHTERPOST PRO00795; GTP_EFTU.
PRINTS; PR00315; ELONGATNFCT.
PR051TE; PS00301; ERACTOR_GTP: 1.
COMPLETE POTCEOME: ELONGATION FACTOR: GTP-binding.
SEQUENCE 394 AA; 42909 MW; 0C571C3D20CBE944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 AA; 43699 MW; 19FCECD3189BCF3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EF-TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2: 1.
Pfam; PF03143; GTP_EFTU_D3: 1.
PRINTS; PR00315; ELONGAINECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00301; EFACTOR_GTP; 1
                                                                                                                                                                                                                                                                                                                                                                                      2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                            3 KEKFERSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TIGR; NMB0124; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=837;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9R420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9R420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RHI2
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Gaps

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Length 395;

ö Gaps ö 87.0%; Score 107; DB 2; Length 395; 85.7%; Pred. No. 3.8e-09; Live 2; Mismatches 1; Indels 395 AA; 43727 MW; B02F39D3173ADA3D CRC64;

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Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000795; GTP_EFTU.
InterPro; IPR0004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF001099; GTP_EFTU_D3. 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATRECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
COMPLETE PROSICEM: ELONGATION factor; GTP-binding.
SEQUENCE 396 AA; 43339 MW; IF58829078B624D2 CRC64;
                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSLATION ELONGATION FACTOR EF-TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ELONGATION FACTOR TU.
87.0%; Score 107; DB 2; Ls
85.7%; Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.0%; Score 107; DB 16; 90.5%; Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AA.
                                                                                                                                                                  396 AA
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                                                                                                                                                                   PRT;
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                                                                                  3 KEHFNRSKPHVNVGTIGHVDH
                                                                    2 KEKFNRTKPHVNIGTIGHVDH
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                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 87.0
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                  Caulobacter crescentus
                        Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                  CC3199 AND CC1240
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC1240;
                                                                                                                                                               Q99QM0,
Q99QM0;
01-JUN-2001 (
                                                                                                                                                                                                                                                                                            Caulobacter
              Query Match
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                                                                                                                                   RESULT
0990M0
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                                                                                                        Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteroides forsythus.
Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                EETU sequence of Porphyromonas gingivalis.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB03465; BAA88138.1; -.
R HSSP; PO2990; IEFU
R InterPro; IPR004161; GTP_EFTU.
R InterPro; IPR004161; GTP_EFTU_D2.
R InterPro; IPR004160; GTP_EFTU_D3.
R Pfam; PF00009; GTP_EFTU, 1.
R Pfam; PF03144; GTP_EFTU_D3; 1.
R Pfam; PF03143; GTP_EFTU_D3; 1.
R Pfam; PF03143; GTP_EFTU_D3; 1.
R PRINTS; PR00315; ELONGATNRCT.
R PROSTITE; PS00310; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 430.7:

A Nagai A., Itoh N.;

Nagai A., Itoh N.;

L "EF-Tu sequence of Bacteroides forsythus.";

L Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB03546; BAA88139.1; -.

R HSSP; PO2990; IEFU.

R InterPro; IPR004161; GTP_EFTU.

R InterPro; IPR004161; GTP_EFTU.D2.

R Pfam; PF00009; GTP_EFTU.D3.

R Pfam; PF03144; GTP_EFTU.D2; 1.

R Pfam; PF03143; GTP_EFTU.D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107; DB 2; Length 395; Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    395 AA; 43669 MW; 1F2F39D3173ADA3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 AA; 43695 MW; 440B33AEE8F39CEF CRC64;
                                  01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
             395 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7
Matches 18; Conservative
           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN-ATCC 33277;
Nagai A., Itoh N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28112;
                                                                                                                                                  NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO 19089 / CB15;

MEDINB-21173698; PubMed-11259647;

Micran W.C., Feldblyum T.V. Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Botocka I., Nelson W.C., Newton A., Stephens C., Phacke N.D., Ely B.,

Potocka I., Nodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

M. Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

M. Viterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

A. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

1. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

REMBL, AE005804; AAK23161.1;

REMBL, AE005999; IETU.
  Gaps
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                     ELONGATION FACTOR TUL
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                                                                                                                                                  SEQUENCE FROM N.A.
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GTP-binding.
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EMBL: AE008652; AAL03546.1; -.
CCMplete proteome.

SEQUENCE 394 AA; 42868 MW; IFBE465785530C63 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 394;
                                                                                    Kong F., Gilbert G.L., "Genomic based mapping and sequencing of U. parvum and U.
                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                              to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               4CB4B2D776A5B145 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                         Score 106; DB 2;
Pred. No. 5.6e-09;
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STRAIN=MALISH 7;
MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                      AF270762; AAK58625.1; -... AF270763; AAK58626.1; -... AF270764; AAK58627.1; -... AF270765; AAK58629.1; -... AF270766; AAK58629.1;
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                                                                                                                                          Submitted (MAY-2000) to the EMI
EMBL: AR270767; AAK58630.1; -.
EMBL: AF270758; AAK58621.1; -.
EMBL: AF270759; AAK58622.1; -.
                                                                                                                                                                                                                    AF270760; AAK58623.1; -. AF270761; AAK58624.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                         86.2%;
90.5%;
Mycoplasmataceae; Ureaplasma
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                    SEQUENCE FROM N.A. STRAIN=VARIOUS STRAIN=
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia conorii.
                   NCBI_TaxID=2130;
                                                                                                                             urealyticum."
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Q9RG55;
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EMBL;
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Q9RG55
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                                                                                                                                                                                                                                                                                             EMBL;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TSO3737; PubMed-110984043;

MEDINE=2043737; PubMed-110984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Rowalik D.J., Lagrou M., Garber R.L., Golltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen":

Nature 406:959-964(2000)

"In Nature 406:959-964(2000)

"In StMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. REMBL, AE004942; ARG07653.1;

"In HSSP; PO2990; 1EFC.

InterProj. 1PR000795; GTP_EFTU.
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Streptomyces mobaraensis.
Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                 STRAIN=ATCC29032;
Olsthoorn-Tieleman L.N., Claij N., Hilgenfeld R., Kraal B.;
Olsthoorn-Tieleman L.N. Claij N., Hilgenfeld R., Ereptomyces
"Elongation factor Tul from the pulvomycin producer Streptomyces
mobaraense is resistant to both pulvomycin and kirromycin.";
EMBL; AFI55617; AAF22606.1; -.
HISSP; P02990; IETU.
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90.5%; Pred. No. 5.6e-09;
iive 0; Mismatches 2; Indels
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PROSTIE; PS00301; EFACTOR_GTP; 1.
Complete proteome; GTP-binding.
SEQUENCE 397 AA; 43369 MW; A019D5BF8BBAB942 CRC64;
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Last annotation update)
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
Pfam; PR00315; BLONGATNFCT.
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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Q97PV3; 097PV3

RESULT 17

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097PV3

Matches

SP1489

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Bohuslavek J., Payne J.W., Liu Y., Bolton H. Jr., Xun L.; "Cloning, Sequencing, and Characterization of a Gene Cluster Involved in EDTA Degradation from the Bacterium BNCI."; Appl. Environ. Microbiol. 67:688-695(2001).
                                                                                                                                                                                                                                                                                            Jr., Xun L.;
iminodiacetate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteriae; Actinobacteria; Actinobacteriae; Actinobacteriae; Actinobacteriae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=55404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olsthoorn-Tieleman L.N., Claij N., Hilgenfeld R., Kraal B.;
"Elongation factor Tul from the pulvomycin producer Streptomyces
mobareance is resistant to both pulvomycin and kirromycin.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF153618; AAF22608.1; -.
EMSSP; POS990: IETU.
InterPro: IRRO00795; GTP_EFTU.
InterPro: IRRO04160; GTP_EFTU_D2.
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                                                                                                                                                                                                                                                                              Liu Y., Louie T. M., Payne J., Bohuslavek J., Bolton H., Identification, purification, and characterization of oxidase from the EDTA-degrading bacterium BNC1."; Appl. Environ. Microbiol. 6:696-701(2001).

EMBL; AF176664; AAG09263.1; -...
INCEPPC: IRRO00795; GTP_EFTU.

PRINTS; PRO0315; ELONGATNFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6B41737CCD77AA6 CRC64;
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Last sequence update)
Last annotation update)
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85.7%; Pred. No. 8.2e-09;
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                                  STRAIN=BNC1;
MEDLINE=21091958; PubMed=11157232;
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                                                                                                                                                                                                                                         STRAIN-BNC1;
MEDLINE-21091959; PubMed-11157233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 AA; 42794 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00315; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KAKFERTKPHVNIGTIGHIDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELONGATION FACTOR TU1.
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     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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Best Local
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09RG53
AC 09RG53,AC 09RG53,AC 09RG53,AC 09RG53,AC 09RG53,AC 00 ACT 01-DEC 0C Bacter 0C Bacter 0C ACT 0C Bacter 0C Bac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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  Length 397;
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                                                        Indels
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004166; GTP_EFTU_D2.
InterPro; IPR004166; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D3; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGANRFCT.
PROSITE; PS00301; EFGCTOR_GTP; 1.
ELONGATE; PR00515; COMPLETE PROTECOME.
SEQUENCE 398 AA; 43970 MW; 5CB2F8F5FA5101A0 CRC64;
                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSLATION ELONGATION FACTOR TU.
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Last annotation update)
Score 106; DB 16;
Pred. No. 5.6e-09;
1; Mismatches 2;
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85.7%; Pred. No. 5.6e-09;
                                                                                                                                                                                                                                                                                      398 AA.
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Bacteria; Proteobacteria; alpha subdivision.
NCBI_TaxID=85561;
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                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-TIGR4;
MEDLINE-21357209; PubMed-11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
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  86.2%;
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Science 293.498-506(2001).
EMBL; AE007444; AAK75581.1;
TIGR; SP1489;
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                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae.
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
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01-DEC-2001
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01-MAR-2001
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RESULT Q9F9S8

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401 AA; 43574 MW; B8ED827C1A717BA0 CRC64;

SEQUENCE

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STRAIR-SEROWAR LAI.
MEDLINE-94014964; PubMed-8409911;
Gravekamp C., Van de Kemp H., Franzen M., Carrington D., Schoone G.J.,
Van Eys G.J., Everard C.O., Hartskeerl R.A., Terpstra W.J.;
"Detection of seven species of pathogenic leptospires by PCR using two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                   Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kormanec J., Nguyen L.D., Novotna J., Knirschova R., Weiser J.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL: AF368284; AAK54131.1; SEQUENCE 397 AA; 43683 MW; BF107EA8036FEF82 CRC64;
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MEDLINE-2008883; PubMed-10620683;
Suerner R.L., Harskeer R.A., van de Kemp H., Bal A.E.;
"Characterization of the Leptospira interrogans S10-spc-alpha
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Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                      Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                 397 AA
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                                                                                                                                   Created)
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                                                                 PRT;
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                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
ELONGATION FACTOR TU.
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Best Local Similarity 85.7;
Matches 18; Conservative
                                                                 PRELIMINARY;
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                                                                                             Q93T39;
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RESULT 20
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                                         Gaps
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Coxiella group; Coxiella.
NCBL_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-NINE MILE PHASE I;
MEDLINE-20002589; PubMed=10531263;
Sabhadri R., Hendrix L.R., Samuel J.E.;
"Differential expression of translational elements by life cycle variants of Coxiella burnetii.";
Infect. Immun. 67:6026-6033(1999).
EMBL; AF136604; AAD32649.1; -.
HSSP; P02990; IEFU.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE ELONGATION FACTOR TU PROTEIN.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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0
 Length 401;
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39448 MW; 4355D7A33B0CCF2C CRC64;
                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
Score 105; DB 2; I
Pred. No. 8.3e-09;
4; Mismatches 0;
                                                                                                                                                                                                     358 AA
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                                                                                                                                                                                                                                         Created)
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InterPro; IPRO004161; GTP_EFTU_D2.
InterPro; IPRO004161; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PRO3143; GTP_EFTU_D3; 1.
PRON1TS; PRO0315; ELONGATNFCT.
GTP-binding.
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SEQUENCE FROM N.A.
STRAIN-1021;
MEDLINE-21368234; PubMed-11474104;
                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                               3 KEKFDRSKPHLNVGTIGHVDH 23
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   85.4%;
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
EF-TU (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobiaceae; Sinorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.73
Matches 18; Conservative
                    Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Coxiella burnetii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=382;
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SEQUENCE
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q925Y6
                                                                                                                                                                                                     09x6G1
                                                                                                                                                                  RESULT 22
Q9x6G1.
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Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; The Complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis ILIA403., Genome Res. 11:731-753(2001).

- I- SINLARIARIY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. EMB.; ARK05959.1; -- HSSP; P02990; IEFU.
                                                                                                                                                                                                                            Moraxella sp. TACII25.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
NCBI_TaxID=103760;
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=TAC II 25, MEDDMED=11112539; MEDLINE-20563866; PubMed=11112539; Masullo M., Arcari P., de Paola B., Parmeggiani A., Bocchini V.; Psychrophilic elongation factor Tu from the antarctic Moraxella sp. Tac II 25: biochemical characterization and cloning of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AJ249258; CAB65285.2; ... HSSP; P02990; 1EFU. InterPro; IPR000795; GTP_EFTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 AA; 43171 MW; 6A1217B78105A1B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) ELONGATION FACTOR TU.
                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.3%; Score 100; DB 2; Le
81.0%; Pred. No. 5.3e-08;
ive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 AA.
                                                               393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                     Created)
                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-IL1403;
MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 39:15531-15539(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004161; GTP_EFTU_22.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRIMTS; PR00315; ELONGATNRCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2001 (TrEMBLrel. 18, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.3
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                 PRELIMINARY;
                                                                                                                                                                                                ELONGATION FACTOR TU
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=TAC II 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arcari P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                            Q9RAJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9CEIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.
              RESULT
                                        Q9RAJ9
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                                                                    HID DESCRIPTION OF SERVICE OF SER
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Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
Cowle A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Rahn D.,
Rahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
Rahn D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
Science 293:668-672(2001).
REMBL, ALS91787; CAC45933.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
STRAIN-CV. JAPONICA NIPPONBARE;
MEDLINE-20062172; Pubwed-10597036;
Lee J.H., Lee J.W., Chung Y.Y., Paek K.H., Shin J.S., Yun C.H.,
Kim J.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 102; DB 16; Length 391;
Pred. No. 2.5e-08;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 AA; 42749 MW; 8846A34F44753693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHLOROPLAST TRANSLATIONAL ELONGATION FACTOR TU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tu cDNA of Oryza sativa L.";
MOI. Cells 9:484-490(1999).
EMBL, AFF45053; AAF15312.1;
HSSP, P07157; IAIP.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KSKFERNKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.9%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 KFERTKPHVNIGTIGHVDH 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.9
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Q9SEF8
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Gaps

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Length 393; Indels

S K D R

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Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Prototheca.
NCBI_TaxID=3111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=263-11;
Knauf U., Hachtel W.;
TA 22 kb fragment of the 53 kb plastid genome of the colourless alga
Prototheka wickerhamii containing atp-, rpl-,rps-, rrn-, and trn-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes.";
Submitted (AUG-1999) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
BIOSYNTHESIS (BY SIMILARITY).
-!- SUBCELULIAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SIMILARITY: BELONG TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AJA45645; CAB53113.1; -.
HSSP; P07157; laip.
                                                                                                                                                                                                                                                                                          SPECIES-S.aureus (strain N315), and S.aureus (strain Mu50);
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.9%; Score 97; DB 16; Length 394; 81.0%; Pred. No. 1.6e-07; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN SYNTHESIS ELONGATION FACTOR TU.
      01-DEC-2001 (TrEMBLrel. 19, Last annotation update) TRANSLATIONAL ELONGATION FACTOR TU.
                                                    TUFA OR SA0506 OR SAV0548.
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain M150).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prototheca wickerhamii.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q9TJQ8;
         DDR READ DR RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloroplast.
Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
                                                                                                                                                                                                                                               Gaps
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-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/ZF-1A SUBFAMILY.
EMBL; AF022186; AAF12934.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20496959; PubMed-11040290;
Glockner G., Rosenthal A., Valentin K.;
"The structure and gene repertoire of an ancient red algal plastid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                              Query Match 80.5%; Score 99; DB 16; Length 395; Best Local Similarity 81.0%; Pred. No. 7.7e-08; Matches 17; Conservative 3; Mismatches 1; Indels
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRAM; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATHFOT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Chloroplast; Elongation factor; GTP-binding; Hypothetical |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.7%; Score 98; DB 8; Length 410; 76.2%; Pred. No. 1.2e-07; Live 3; Mismatches 2; Indels
                                                                                        C8D138A5147213F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 AA; 44731 MW; 66862440F7D54B65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 44.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created),01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
InterPro; IPR000795; GTP_EFTU. PRINTS; PR00315; ELONGATNECT. Complete proteome; GTP-binding. SEQUENCE 395 AA, 43212 MW; G
                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                     3 KEVYDRSKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RAKFERSKPHINIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 76.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyanidium caldarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02990; 1EFU.
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Tu cDNA."
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                                                                                                                            Gaps
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            Nicotiana sylvestris (Wood tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                       Brandt P., Fartmann B., Holland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01, Created)
TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
ELONGATION FACTOR TUR (EF-TUR) PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 3; Length 437; Pred. No. 1.8e-07; 0; Mismatches 1; Indels
                                                                                                       Score 97; DB 8; Length 409;
Pred. No. 1.7e-07;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AL513467. CAC28833.1;
HSSP; P02990; 1EFU.
InterPro; IPR000795; GTP_EFTU.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00310; EFACTOR_GTP; 1.
Elongation factor; GTP-binding; Protein biosynthesis.
SEQUENCE 437 AA; 47848 MW; 2F64E769FE7CEE35 CRC64;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B. Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                           01-JUN-2001 (TremBirel. 17, Created)
01-JUN-2001 (TremBirel. 17, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
PROBABLE TRANSLATION ELONGATION FACTOR EF-TU PRECURSOR, MITCCHONDRIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 AA
                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
         IPR004161; GTP_EFTU_D2. IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
InterPro; IPR000795; GTP_EFTU.
                                                                                                                                                      RAKFERKKPHVNIGTIGHVDH 23
                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                         78.9%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.9%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 FNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 FQRTKPHVNIGTIGHVDH 58
                                                                                                         Query Match 78.9°
Best Local Similarity 81.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                  Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q40450;
01-NOV-1996 (
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01-DEC-2001
CHLOROPLAST E
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Q40450
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HSSP; PUZJUS, IEFU.
INTERPROS, IPRO0795; GTP_EFTU.
INTERPROS, IPRO04160; GTP_EFTU_D2.
INTERPROS, IPRO04160; GTP_EFTU_D2.
Ffam; PP003144; GTP_EFTU_D2; 1.
Pfam; PP03144; GTP_EFTU_D2; 1.
Pfam; PP03143; GTP_EFTU_D3; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; GTP-binding; Protein biosynthesis; Transit peptide.
TRANSIT 1 70 POTENTIAL.
                                                                                                                                                                                                   Murayama Y., Matsubayashi T., Sugita M., Sugiura M.;
"Purification of chloroplast elongation factor Tu and cDNA analysis in tobacco: the existence of two chloroplast elongation factor Tu species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDINE-20550852; PubMed=11101151; MEDINE-20550862; PubMed=11101151; Kang C.J., Lee M.G., Cho Y.S., Lee J.W., Kyung Y.J., Shin J.S., Kim E.S., Kim E.S., Kim G.S., Telmaracterization of geranium (Pelargonium graveolens) chloroplast EF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pelargonium graveolens (rose geranium).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Geraniales; Geraniaceae; Pelargonium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 457;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004166; GTP_EFTU_D2.
Pfam; PF00009; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTE; PR00315; ELONGATNRCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; GTP-binding; Protein biosynthesis.
SEQUENCE 474 AA; 51315 MW; A321742468553865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8A30C50DC137F755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHLOROPLAST TRANSLATIONAL ELONGATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.0%; Score 96; DB 10; L. 89.5%; Pred. No. 2.8e-07; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 AA.
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                                                                                                                                                                                                                                                                                                                              Plant Mol. Biol. 22:767-774(1993).
EMBL; D11375; BAA01974.1; -.
HSSP; P02990; 1EFU.
                                                                                                                                                                                    MEDLINE=93363910; PubMed=8358028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO1. Cells 10:579-583(2000).
EMBL; AF234537; AAK08141.1;
HSSP; P02990; IEFU.
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hes 17; Conservative
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457 AA;
                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE=93363910; PubMed=8358028;
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                    Query Match
Best Local
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Q95TV3
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                                                                                                                                                                                                                                                                                                      Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Mayers M.C., Miranda M., Narusska M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shino P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIANE-94373864; PubMed-8087886;
Sugita M., Murayama Y., Sugiura M.;
"Structure and differential expression of two distinct genes encoding
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana sylvestris (Wood tobacco).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.0%; Score 96; DB 10; Length 476; 89.5%; Pred. No. 2.9e-07; 1ve 0; Mismatches 2; Indels
             Length 474;
Score 96; DB 10; Length 4//
Pred. No. 2.9e-07;
                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE CHLOROPLAST TRANSLATION ELONGATION FACTOR BF-TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                         476 AA; 51656 MW; 77B38DD1BB5386A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHLOROPLAST ELONGATION FACTOR TUB(EF-TUB) PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the chloroplast elongation factor Tu in tobacco.";
                                                                                                                                          476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 AA
                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                          PRT;
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            78.0%;
89.5%;
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                                                         4 KFNRTKPHVNIGTIGHVDH 22
                                                                       4 KFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Elongation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
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SEQUENCE FROM N.A.
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TISSUE=TOUNG LEAF;
                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
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                                   Matches
                                                                                                                   RESULT 33
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Murayama Y., Matsubayashi T., Sugita M., Sugiura M.;
"Purification of chloroplast elongation factor Tu and cDNA analysis in tobacco: the existence of two chloroplast elongation factor Tu species.";
                                                                                                                                                                                                                                                                                                                                                                                                                     Elongation factor; GTP-binding; Protein biosynthesis; Transit peptide. TRANSIT 1 77 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewisls S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AY058493; AAL13722.1; -.
SEQUENCE 300 AA; 32987 MW; BECF21E546FBCDCA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHLOROPLAST ELONGATION FACTOR TUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.2%; Score 95; DB 5; Length 300; 76.2%; Pred. No. 2.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EF-TUB).
FE88EF5D48B92D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GM14682P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 96; DB 10;
Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                            Plant Mol. Biol. 22:767-774(1993).
EMBL: D11470; BAA012038.1; -
EMBL: D11376; BAA01975.1; -
HSSP; P029390; HEFU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2: 1.
Pfam; PF03144; GTP_EFTU_D2: 1.
PRINTS; PR03143; GTP_EFTU_D3: 1.
PRINTS; PR03143; GTP_EFTU_D3: 1.
PRINTS; PR03143; GTP_EFTU_D3: 1.
PRINTS; PR03143; GTP_EFTU_D3: 1.
PROSITE; PS03315; ELONGAINFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9V6Q7;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 KFERKKPHVNIGTIGHVDH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.2
Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 89.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485
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119 AA

PRT;

PRELIMINARY;

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Apicomplexans.";
Profilst 149:51-59(1998).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
BIOSYNTHESIS (BY SIMILARITY).
-!- SUBCELLIDIAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y11429; CAA72237.1; -.
HSSP; P02990; 1EFU.
InterPro; IPR000795; GTP_EFTU.
Pfam; PR00009; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNRCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Chloroplast; Elongation factor; GTP-binding; Protein biosynthesis.
                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                                                                  Denny P., Preiser P., Williamson D., Wilson I.; "Evidence for a single origin of the 35 kb plastid DNA in
                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ELONGATION FACTOR TU (FRAGMENT).
                                                                                                                                                                                                                        Theileria annulata.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5874;
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                                                                                                                                                                                                                                            Chloroplast.
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SEQUENCE
                                                                                                       078381;
                                                                                078381
                                         RESULT
078381
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                                                                                                       RC STRAIN-BERKELEY.

RX MEDICHCE FROM N.A.

RADAIN-BERKELEY.

RA Adams M.D. Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

RA Adams M.D. Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

RA Adams M.D. Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.C., Champe M., Pfelffer B.D.,

RADILJ J.F., Agbayan A., An H.J., Andrews-Frannkoch C., Baldwin D.,

RADILOW B. Botchan M. Baxendall J., Baytaktaroglu L., Beasley E.M.,

RADERON K.Y., Beans P.V., Berman B.P., Bhandari D., Bolshakov S.,

Burtis N.C., Busam D.A., Bulter H., Caddeu E., Center A., Chandra I.,

RADAGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RADOGON K., Malshan A.E., Gargu D.S., Gelbart W.M., Glasser K.,

Allali M., Kalush F., Karpen G.H., Re Z., Kenipason J.A., Retchum K.A.,

Allali M., Malush F., Karpen G.H., Re Z., Kenipason J.A.,

RADOR D., Leilar V., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RADOR D., Leilar V., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RADOR D., Leilar W., Wobbarry C., Morris J., Moshrefi A.,

RODOR S., Woly M., Wurphy B., Wontep W., Strong R., Steleler F., Shen H.,

Rabor D., Leilar V., Evangeler M., Ressenbach J.,

Rador S., Spadding A.C., Standers R., Venter E., Wang X., Wang X.,

Rador S., Wollow R., Worley R.W., Rollon G., Zhan M., Zhong W., Zhon G., Zhan M., Zhong W., Zhon S., Zhan M., Zhong S., Zho O., Zhan S., Rador S., Zhan S., Rador S., Zhan S., Scheeler F., Spaceler F.,
                                                     Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP-binding; Protein biosynthesis.
SEQUENCE 489 AA; 53992 MW; 9D09C36C4AEB2EE1 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
EMBL: AE003018: AAFS8366.1; --
HSSP: P02990; lETU.
FlyBase: FBGn0024556; EfTuM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conservat
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                      01-DEC-2001 (T:
CG6050 PROTEIN
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                          ö
Query Match 76.4%; Score 94; DB 8; Length 119; Best Local Similarity 71.4%; Pred. No. 1.3e-07; Matches 15; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                  396 AA.
                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                              22
                                                                                                  3 KKQFLRNKPHINIGTIGHIDH
                                                                              2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                             ELONGATION FACTOR TU.
XF2640 AND XF2628.
                                                                                                                                                                                                                                                                                                                                                       Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-9A5C
                                                                                                                                                                                                                                                                                                                                                                                           Xylella
                                                                                                                                                                                                                                      09P909;
                                                                                                                                                                                                                  09P909
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Gaps .; 0

Score 95; DB 5; Length 489; Pred. No. 4.4e-07; 2; Mismatches 3; Indels

7

16; Conservative

77.2%; 76.2%;

2 KEKFNRTKPHVNIGTIGHVDH 22

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119 AA; 13312 MW; 122F230BC0340BEC CRC64;

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Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Marino C.L.,

Machado M.A., Mardeira A.M.B.N., Madeira H.M.F., Matsukuma J.Y.,

Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

Marques M.V., Mardins E.A.L., Martins E.M.F., Paris A.,

Moon D.H., Nagaim M.R., Oliveira M.A.,

Mardina A.G., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,

A Silva A.C.K. da Silva A.M., da Silva M.A. Jr. de Souza A.A.,

A da Silva A.C.K., da Silva M.M.L.Z., Siqueira W.J., de Souza A.B.,

A da Silva A.C.K., da Silva M.M., Verjoxki-Indmedda S., Vettore A.L.,

A da Silveira J.F., Silvestri M.A., Verjoxki-Indmedda S., Vettore A.L.,

A da Silva M.A., Zatz M., Weidanis J., Setubal J.C.;

"The genome sequence of the plant pathogen Xylella fastidiosa.";

"The genome sequence of the plant pathogen Xylella fastidiosa.";

"The genome sequence of the plant pathogen Xylella fastidiosa.";

"The genome sequence of the plant pathogen Xylella Fastidiosa.";

"The genome sequence of the plant pathogen Xylella Fastidiosa.";

"The genome sequence of the plant pathogen Xylella Fastidiosa.";

"The genome sequence of the plant pathogen Sylella Fastidiosa.";

"The genome sequence of the plant pathogen Sylella Fastidiosa.";

"The genome sequence of the plant pathogen Sylella Fastidiosa.";

"The genome sequence of the plant pathogen Sylella Fastidiosa.";

"The genome Sequence of the plant pathogen Sylella Fastidiosa.";

"The genome Sequence of the plant pathogen Sylella Fa
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"Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
J. Bacteriol. 183:1853-1861(2001).
BENBL, AF274444; AAK17080.1;
HSSP: P07157; IAPP.
InterPro: IPR0004161; GTP_EFTU.
InterPro: IPR004161; GTP_EFTU.
InterPro: IPR004161; GTP_EFTU.
Pfam: PF03144; GTP_EFTU.22:
Pfam: PF03144; GTP_EFTU.22:
InterPro: IPR0344; GTP_EFTU.22:
IPR0344; GTP_EFTU.23:
IPR0344; GTP_EFTU.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Candidatus Carsonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.4%; Score 94; DB 16; Length 396; 76.2%; Pred. No. 5e-07; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44056 MW; 2524B4E2BD62E062 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FINGRATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21125546; PubMed=11222582;
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PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QDKFKRTKLHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candidatus Carsonella ruddii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH
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Best Local Similarity 76.2°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding
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Q9AIG6
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Toxoplasma.
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"An elongation factor encoded by the toxoplasma gondii putative
plastid.";
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76.2%; Pred. No. 5.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elongation factor; GTP-binding; Protein biosynthesis. SEQUENCE 401 Aa; 44294 MW; C7C8B9F3ACF7530F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
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Copyright (c) 1993 - 2000
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    protein search, using sw model

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elongation Factor Tu (Ef-Tu) [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: H97285 R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R.; L. J. Barteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUD:21359325; PMID:21359325 A;Reference comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUD:21359325; PMID:21359325 A;Coression: H97285 A;Coresion: L397 <cur>
A;Coresion: Coresion: A;Coresion: A;Coresion: Clostridium acetobutylicum ATCC824 A;Coresion: Coresion: Coresion: A;Cores: Clostridium acetobutylicum ATCC824 A;Gene: CAC3136 A;Cores: Coresion: Coresi
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N;Contains: GTPase (EC 3.6.1..)

N;Contains: GTPase (EC 3.6.1..)

C;Species: Escherichia coli

C;Species: Bscherichia coli

C;Accession: A91478, A91095; A92332; I58035; G65204; A03518; A91475

R;Ah, G; Friesen, J.D.

Gene 12, 33-39, 1980

A;Title: The nucleotide sequence of tufB and four nearby tRNA structural genes of Esc
A;Reference number: A91478; MUD: 8116558

A;Reference number: A91478; MUD: 8116558

A;Residues: 1-394 <ANG;
A;Cross-references: GB:J01717; NID: 9147968; PIDN:AAA24669.1; PID: 9147969

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A;Cross-reference number: A91095; MUD: 81003875

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A;Accession: A92332; MUD: 81264196

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R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
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A; Accession: G65204
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95.2%; Pred. No. 2.6e-09;
ive 0; Mismatches 1; Indels
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A;Accession: 158035
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A;Residues: 1-13 <RES>
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A; Residues: 2-394 cLAU-
R; Hudson, L:; Rossi, J:; Landy, A.
Nature 294, 422-427, 1981
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Matches 20; Conserv
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C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo C; Superfamily: translation elongation factor Tu prop; protein biosynthesis C; Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis F:13-139/Domain: translation elongation factor Tu homology <ETU>F; 19-26/Region: nucleotide-binding motif A (P-loop)
F:136-139/Region: GTP-binding NKXD motif F:136-139/Region: GTP-binding SAK/L motif F:174-176/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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C; Accession: E64670
C; Accession: E64650
C; Accession: E64650
C; Accession: E64650
C; Accession: E64650
C; MULLo, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Reference number: A64520; MULD: 97394467
A; Reference number: A64520; MULD: 97394467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accessive ferences: GB.AE000626; GB.AE000511; NID:g2314360; PIDN:AAD08250.1; PID:g231436 (S.Superfamily: translation elongation factor Tu; translation elongation factor Tu homology (S.Superfamily: translation elongation factor Tu; translation elongation factor Tu homology (S.Superfamily: translation elongation factor Tu homology (ETU) (S.Superfamily: Translation elongation elongation factor factor Tu homology (ETU) (S.Superfamily: The Manual ETI) (S.Superfamily: The Manual 
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(Species: Bacteroides fragilis
(Species: Bacteroides fragilis
(Species: Bacteroides fragilis
(Species: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 02-Feb-2001
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(Arthe: Complete nucleotide sequences of seven eubacterial genes coding for the elongat Arther: Complete nucleotide sequences of seven eubacterial genes coding for the elongat Arther: not compared with conceptual translation
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 02-Feb-2001
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in 0%; Pred. No. 3.2e-10;
--inhas 0;
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Pred. No. 2.6e-09;
); Mismatches 1;
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100.08; P.V.
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Best Local Similarity 95.2
Matches 20; Conservative
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Residues: 1-399 <TOM>
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Residues: 1-394 <LUD>
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A.Map position: 74 min
A.Start codon: GTG
A.Start codon: GTG
A.Start codon: GTG
C.Function:
C.Superfamily: translation elongation factor Tu: translation elongation factor Tu hom
C.Superfamily: translation elongation factor Tu #status experimental <AMI>C.F.19-26/Region: uncleotide-binding motif A (P-loop)
F.13-139/Region: GTP-binding NKXD motif
F.174-176/Region: GTP-binding SAK/L motif
F.174-176/Region: GTP-binding site: Mg-GTP (Lys, Thr, Asn, Lys, Asp, Ser) #
F.55/Modified site: NG-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #status e
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A; Residues: 1-394 <BLAT>
A; Residues: 1-394 <BLAT>
A; Residues: 1-394 <BLAT>
A; Cross-references: GB.AED00410; GB:U00096; NID:g1789734; PIDN:AAC76364.1; PID:g17897
A; Cross-references: GB.AED00410; GB:U00096; NID:g1789734; PIDN:AAC76364.1; PID:g17897
A; Kawashima, T.; Berthet-colominas, C.; Wulff, M.; Cusack, S.; Leberman, R.
submitted to the Brookhaven Protein Data Bank, July 1996
A; Reference number: A65506; PDB:IEFC
A; Contents: annotation; X-ray crystallography, 2.5 angstroms
B; Kawashima, T.; Colominas, C.B.; Wulff, M.; Cusack, S.; Leberman, R.
Nature 379, 511-518, 1996
A; Contents: annotation of the Escherichia coli EF-Tu.EF-Ts complex at 2.5angstroms re
A; Reference number: A58848; WUID:96170031
A; Contents: annotation; X-ray crystallography, 2.5 angstroms
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
C;Genetics:
                                                                             A; Molecule type: protein
A; Residues: 60.264 <a href="Annals-align: red">A; Residues: 60.264 <a href="Annals-align: red">A; Residues: 60.264 <a href="Air annals-align: red">A; Note: this portion of the molecule was designated fragment B
A; Bottion of F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Science 277, 1453-1462, 1997
A; Fitle: The complete genome sequence of Escherichia coli K-12.
A; Fitle: The complete genome sequence of Escherichia coli K-12.
A; Accession: F65127
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
C;Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F;13-139/Domain: translation elongation factor Tu homology FTU
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A;Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 3.7e-09;
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A; Reference number: A61304; MUID:82189911
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90.5%;
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Best Local Similarity
Matches 19; Conserv
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A; Residues: 1-394 <TUO>
A; Cross-references: EMBI
                                        A; Accession: A61304
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A;Gene: tufA; strD
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                           A; Molecule type: DNA
A; Residues: 1-394 < CLAN
A; Cross-references: GB:AE000472; GB:U00096; NID:g2367333; PIDN:AAC76954.1; PID:g1790412;
A; Experimental source: strain K-12, substrain MG1655
B; Kawashima, T.; Berthet-colominas, C.; Wulff, M.; Cusack, S.; Leberman, R.
B; Kawashima, T.; Colominas, C.B.; Wulff, M.; Cusack, S.; Leberman, R.
A; Rontents: annotation; X-ray crystallography, 2.5 angstroms
B; Rawashima, T.; Colominas, C.B.; Wulff, M.; Cusack, S.; Leberman, R.
B; Rawashima, T.; Colominas, C.B.; Wulff, M.; Cusack, S.; Leberman, R.
B; Rawashima, T.; Colominas, C.B.; Wulff, M.; Cusack, S.; Leberman, R.
B; Rawashima; T.; Sangstroms resol
A; Reference number: A58848; MUID:96170031
A; Reference number: A58848; MUID:96170031
A; Contents: annotation; X-ray crystallography, 2.5 angstroms
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J. Biochem. 91, 1047-1063, 1982
A;Title: Primary structure of the polypeptide chain elongation factor Tu from Escherichi
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Eur. J. Balochen. 108, 507-526, 1980
A;Title: The complete amino-acid sequence of elongation factor Tu from Escherichia coli.
A;Reference number: A91095; MUID:81003875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 2-394 <JONS
R;Laursen, R.A.; L'Italien, J.J.; Nagarkatti, S.; Miller, D.L.
J. Bloot. Chem. 256, 8102-8109, 1981
A;Title: The amino acid sequence of elongation factor Tu of Escherichia coli. The comple
A;Reference number: A92332; MUID:81264196
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N.Contains: GTPase (EC 3.6.1.)
C;Species: Escherichia coli
C;Date: 30-Nov-1980 * sequence_revision 09-Jun-1994 * text_change 19-Jan-2001
C;Accession: A914/75; B91095; B92332; A61304; F65127; A03518; A91478
R;Yokota, T.; Sugisaki, H.; Takanami, M.; Kaziro, Y.
Gene 12, 25-31, 1980
A;Title: The nucleotide sequence of the cloned tufA gene of Escherichia coli.
A;Reference number: A91475; MUID:81165557
preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-394 <YOK>
A;Cross-references: GB:J01690; NID:g147889; PID:g147897
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Best Local Similarity 90.5
Matches 19; Conservative
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A;Map position: 90 min
A;Start codon: GTG
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Drotein chain elongation factor EF-Tu [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: G91241

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: G91241

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <HAX>
A;Residues: 1-394 <HAX>
A;Cross-references: GB:BA000007; PIDN:BAB38326.1; PID:g13364379; GSPDB:GN00154
C;Genetics: A;Gene: ECS4903
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                     Alote: two copies of this gene are found in the Haemophilus influenzae chromosome C; Superfamily: translation elongation factor Tu; translation elongation factor Tu c. Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis F;13-139/Domain: translation elongation factor Tu homology <ETU> F;19-26/Region: nucleotide-binding motif A (P-loop) F;13-139/Region: GTP-binding NKXD motif F;174-176/Region: GTP-binding SAK/L motif F;25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #
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A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A; Reference number: A99629; MuID:21156231; PMID:11258796
A; Recession: F91152
A; Status: presliminary
A; Molecule type: DNA
A; Residues: 1-394 < HAY>
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: F91152
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90.5%; Pred. No. 3.7e-09;
....omatches 1;
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Matches 19; Conserv
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C;Species: Haemophilus influenzae
C;Species: Haemophilus
C; Haemophilus influenzae
C; Haemophilus influenzae
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C; Hae
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C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
C; Superfamily: translation elongation factor Tu homology cFTU>
C; Superfamily: translation elongation factor Tu homology cFTU>
F; 13-139/Domain: translation elongation factor Tu homology cFTU>
F; 19-26/Region: nucleotide-binding motif A (P-loop)
F; 136-139/Region: GTP-binding NXXD motif
F; 136-136/Region: GTP-binding SXX/L motif
F; 25, 26, 62, 136, 137, 139, 174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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C.Species: Salson
S.Societa Salson
S.Tateranslation S., Gesteland, R.F.; Hughes, D.; Atkins, J.F.
Blochim. Blochyns. Acta 1050, 274-278, 1990
A.Title: The role of EF-Tu and other translation components in determining translocation
A.Reference number: S13560; MUID: 91002658
A.Accession: S13560
A.Status: nucleic acid sequence not shown; translation not shown
A.Sesidues: 1-394 <TUO>
A.Residues: 1-394 <TUO>
A.Residues: 1-394 <TUO>
A.Residues: 1-394 <TUO>
C.Genetics:
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rA;Residues: 1-394 <TIG2>
A;Cross'references: GB:U32746; GB:L42023; NID:g1573626; PIDN:AAC22292.1; PID:g1573634;
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F:19-26/Region: nucleotide-binding motif A (P-loop)
F:136-139/Region: GTP-binding NKXD motif
F:174-176/Region: GTP-binding SAK/L motif
F:25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Asn,
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Pred. No. 3.7e-09;
1; Mismatches 1;
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Pred. No. 3.7e-09;
                                                                                                                                                                                                                                                                                                                              1; Mismatches
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Best Local Similarity 90.59
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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C;Species: Yersinia pestis
C;Date. 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0457
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. Ancherraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Davies, G.M.; Davis, P.; Davis, B.M.; Davis, P.; Davis, B.M.; Davis, P.; Davis, G.; Barrelli, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AE0025
R;Parkhilly J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarknaga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
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                                                                                                                                                    hypothetical protein tufB [imported] - Escherichia coli (strain O157:H7, substrain
                                                                                                                                                                                                                                       C, Accession: D86089
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.;
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.;
iller, E.; Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Accession: D86089
A; Accession: D86089
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 <STO>
A; Forsidues: Teferences: GB: AE005174; NID: 912518902; PIDN: AAG59176.1; GSPDB: GN00145; IA; Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:ALS90842; PIDN:CAC93222.1; PID:g1S981670; GSPDB:GN00175 C;Genetics: A;Gene: tufa C;Superfamily: translation elongation factor This translation elongation el
                                                                                                                                                                                              C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0457
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90.5%; Pred. No. 3.7e-09;
iive 1; Mismatches 1;
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Pred. No. 3.7e-09;
1; Mismatches 1;
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90.5%;
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Best Local Similarity
Matches 19; Conserv
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A;Molecule type: DNA
A;Residues: 1-394 <KUR>
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Matches 19; Conserv
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C; Genetics:
A; Age position: 1
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE004124; GB:AE003852; NID:g9654770; PIDN:AAF93535.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
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C; Species: Vibrio cholerae
C; Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: G8237
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Makalanons, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                            translation elongation factor EF-Tu VC0362 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: D82332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rifieldelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
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    Length 394;
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Pred. No. 3.7e-09;
1; Mismatches 1; Indels
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Score 111; DB 2;
Pred. No. 3.7e-09;
1; Mismatches 1;
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Pred. No. 3.7e-09;
1; Mismatches 1.
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90.2%;
90.5%;
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Best Local Similarity 90.5%;
Matches 19; Conservative
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nilarity 90.5%;
Conservative
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A;Residues: 1-394 <HEI>
A;Cross-references: GB:AE004120;
                                                                              Conservative
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Best Local Similarity
                                         Local Similarity
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    Query Match
                                         Best Loca
Matches
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C; Species: Listeria monocytogenes
C; Species: Listeria monocytogenes
C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AD1406
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Accession: AD1406
A; Accession: AD1406
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-395 cdLA>
A; Cross-references: GB:NC_003210; PIDN:CAD00866.1; PID:g16412153; GSPDB:GN00177
A; Experimental source: strain EGD-e
C; Genetics:
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A; Checkics: Listeria appearation elongation factor Tu hom
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                                     C; Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu
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C;Genetics:
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                                                                                                                                                                                                                                             Indels
                                                                                                                                                         Score 111; DB 2; L. Pred. No. 3.7e-09; 1; Mismatches 1;
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Pred. No. 7.4e-09;
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ilarity 90.5%;
Conservative
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90.5%;
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 <PAR>
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Best Local Similarity
        A; Gene: tufB
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C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: 85998
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Aritle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A88480; MUID:21074935; PMID:11206551
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A; Molecule type: DNA
A; Residues: 1-394 <STO>
A; Residues: 1-394 <STO>
A; Cross-references: GB: AE005174; NID: 912517957; PIDN: AAGS8446.1; GSPDB: GN00145; UWGP: Z46
A; Experimental source: strain 0157: H7, substrain EDL933
C; Genetics:
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A;Gene: tufA
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
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R; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, P. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Atthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; PMID:11677608
A; Reference number: AB0502; PMID:11677608
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                                                                                                            A; Accession: AE0025
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 < KUR>
A; Cross-references: GB: AL590842; PIDN: CAC89064.1; PID: 915978304; GSPDB: GN00175
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-394 < PAR>
A; Cross. references: GB: AL513382; PIDN: CAD09494.1; PID: g16504611; GSPDB: GN00176
C; Genetics:
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                                     A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
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Pred. No. 3.7e-09;
1; Mismatches 1; Indels
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Pred. No. 3.7e-09;
1; Mismatches 1; Indels
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Best Local Similarity 90.5%;
Matches 19; Conservative
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Best Local Similarity 90.5%;
Matches 19; Conservative
Nature 413, 523-527, 2001
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C; Species: Brucella melitensis (st. Species: Older St. 
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
F;13-139/Domain: translation elongation factor Tu homology <ETU>
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A;Experimental source: serotype O2, strain NCTC 11168
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R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A; Reference number: A81250; MUD: 20150912
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-399 <PAR>
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A; Residues: 1-391 <KUR>
A; Cross-references: GB:AE008917; PIDN:AAL51936.1; PID:g17982694; GSPDB:GN00190
A; Experimental source: strain 16M
C; Genetics: _____
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C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
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90.5%; Pred. No. 1.1e-08;
tive 1; Mismatches 1;
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2 KEKFNRTKPHVNIGTIGHVDH
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Best Local Similarity 90.5
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C; Superfact
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R:Rowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Blod. Rep. 13, 336-342, 1995
A.Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensi
A.Feference number: S78238
A.Feference number: S78248
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Status: DNA
A.Fesiques: 1-409 < KCWA>
A.Status: DNA
A.Fesiques: 1-409 < KCWA>
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 9185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PIDN: CAA91621.1; PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PID: PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PID: PID: 91185138
A.Gross-references: EMBL: Z67753; NID: 91185127; PID: PID: 91185127; PID: 91185138
A.Gross-references: EMBL: PID: 9118513
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Bominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1782
A; Molecule type: DNA
A; Residues: 1-395 GGLA>
A; Cross-references: GB:AL592022; PIDN:CAC98028.1; PID:g16415338; GSPDB:GN00178
A; Residues: 1-395 GGLA>
A; Cross-references: CB:AL592022; PIDN:CAC98028.1; PID:g16415338; GSPDB:GN00178
A; Residues: Lufa
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolc
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AD1782
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche,
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C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 02-Feb-2001
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         Indels
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    Mismatches
    7
                                                                                                                                            3 KEKFDRSKPHVNIGTIGHVDH 23
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Matches 19; Conservative
    Conservative
19;
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    Matches
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translation elongation factor Tu NMB0124 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: A81235; D82006; C82008
R;Tettellin, H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Uthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Itle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
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A;Molecule type: DNA
A;COSS-references: 1-34
A;COSS-references: GB:AE002371; GB:AE002098; NID:g7225337; PIDN:AAF40583.1; PID:g722
A;Experimental source: serogroup B, strain MC58
B;Parkhill, J; Achtman, M; James, K.D; Benley, S.D; Churcher, C.; Klee, S.R; Mo
Holroyd, S.; Jagels, K; Leather, S.; Moule, S.; Mungall, K.; Quall, M.A.; Rajandre
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A;Accession: D82006
                 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Teference number: A81000; MUID:20175755
A;Accession: D81234
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A;Molecule type: DNA
A;Residues: 1-394 <PRAN
A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83449.1; PID:g737
A;Experimental source: serogroup A, strain 22491
A;Accession: C82008
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A, strain Z2491
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J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu
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A;Experimental source: serogroup B, strain MC58
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C;Superfamily: translation elongation factor Tu; translation elon
F;13-139/Domain: translation elongation factor Tu homology <ETU>
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Pred. No. 1.5e-08;
2; Mismatches 1; Indels
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Pred. No. 1.5e-08;
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85.78;
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A; Experimental source: serogroup
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <TET>
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Best Local Similarity
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                                                        A. Variety: ATCC 50394
C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C; Accession: 578139
C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C; Accession: 578139
R; Lang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank Nature 387, 493-497, 1997
A; Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniature.
A; Reference number: 578127; MUD:97311393
A; Accession: 578139
A; Accession: 578139
A; Accession: 578139
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-394 cLAN>
A; Cross-references: EMBL:AF007261; NID:92258325; PIDN:AAD11872.1; PID:92258338
A; Experimental source: ATCC 50394
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997
C; Genetics:
A; Gene: tufA
A; Gene: mitochondrion
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu; homology cFTU>
C; Reywords: GFP binding; methylated amino acid; mitochondrion; nucleotide-binding motif A (P-loop)
F; 13-139/Domain: translation elongation factor Tu; homology cFTU>
F; 19-56/Region: nucleotide-binding sak/L motif F; 174-176/Region: GTP-binding sak/L motif F; 174-176/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #states F; 57/Modified site: N6-methyllysine or N6, N6-dimethyllysine (Lys) #status predicted
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:Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
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C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C; Date: 02-Jun-2000
C; Date: 02-Jun-2
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ilarity 85.7%; Pred. No. 1.5e-08;
Conservative 2; Mismatches 1;
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llarity 90.5%; Pred. No. 1.5e-08;
Conservative 0; Mismatches 2;
                                      Species: mitochondrion Reclinomonas americana
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Best Local Similarity
Matches 19; Conserv
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Matches 18; Conserv
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Ribelvechio, V.G.: Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov R. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUD:99287316
A;Recession: G72243
A;Molecule type: DNA
A;Residues: 1-400 <ARN>
A;Cross-references: GB:AE001799; GB:AE000512; NID:94982067; PIDN:AAD36569.1; PID:9498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental Source: strain MS, Statter, K.O.; Schleifer, K.H.
FEMS Microbiol. Lett. 57, 115-120, 1989
A; Title: Nucleotide sequence of the gene coding for the elongation factor Tu from the A; Reference number: A48314
A; Accession: A48314
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
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                                                                                                                                                                                                                               C; Species: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Feb-2001
C; Accession: G72243; A48314 A48314, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Argene: TM1502
C; Superfamily: translation elongation factor Tu; translation elongation factor C; Superfamily: translation elongation factor C; Superfamily: translation elongation F: 13-139/Domain: translation elongation factor Tu homology <eTU>
F: 13-139/Domain: translation elongation factor Tu homology <eTU>
F: 13-26/Region: nucleotide-binding motif A (P-loop)
F: 136-139/Region: GTP-binding NMXD motif
F: 174-176/Region: GTP-binding SAM/L motif
F: 25, 26, 62, 136, 137, 139, 174/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp,
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AH3344
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                                                                                                                                                                                                      translation elongation factor EF-Tu – Thermotoga maritima (strain MSB8)
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85.7%; Pred. No. 1.5e-08;
ive 2; Mismatches 1; Indels
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A, Cross-references: GB:AE008917; P
A, Experimental source: strain 16M
C, Genetics:
A, Gene: BME10742
   2 KEKFNRTKPHVNIGTIGHVDH
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Best Local Similarity 85.7
Matches 18; Conservative
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A;Molecule type: DNA
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A.Residues: 1-396 <BRED
A.Across-references: EMBL:X82820; NID:g609255; PIDN:CAA58029.1; PID:g609256
A.Koross-references: EMBL:X82820; NID:g609255; PIDN:CAA58029.1; PID:g609256
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
C.Superfamily: translation elongation factor Tu: translation factor Tu homology (Keywords: GTP binding; nucleotide binding; P-loop
F.13-139/Domain: translation elongation factor Tu homology <ETU>
F.19-26/Region: nucleotide-binding motif A (P-loop)
F.136-139/Region: GTP-binding SAK/L motif
F.174-176/Region: GTP-binding sak/L motif
F.25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20.Apr-2001 #sequence_revision 20.Apr-2001 #text_change 18-Jul-2001
C;Accession: A87403; E87464
E;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B;Iaub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4135-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                              R'Bremaud, L.; Fremaux, C.; Laalami, S.; Cenatiempo, Y.
Nucleic Acids Res. 23, 1737-1743, 1995
A'Itle: Genetic and molecular analysis of the tRNA-tufB operon of the myxobacterium Sti
A;Reference number: $55281; MUID:95303606
A;Accession: $55281
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
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A;Cross-references: GB:AE005673; NID:913422569; PIDN:AAK23221.1; GSPDB:GN00148
A;Accession: E87645
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A;Residues: 1-396 <ST2>
A;Cross-references: GB:AE005673; NID:913424877; PIDN:AAK25161.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                 translation elongation factor EF-Tu - Stigmatella aurantiaca
C;Species: Stigmatella aurantiaca
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 02-Feb-2001
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Pred. No. 1.5e-08;
0; Mismatches 2; Indels
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90.5%; Pred. No. 1.5e-08;
tive 0; Mismatches 2;
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   Mismatches
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90.5%;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S55281; S52237
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I.; Holroyd,
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A;Accession: H70639
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A;Experimental source: strain H37Rv
C;Genetics:
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
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Cispecies: Rickettsia conorii Rolliani H97825
Rickettsia P. F. Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2094, 2001
A;Fitle: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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A; Residues: 1-396 < CAR>
A; Residues: 1-396 < CAR>
A; Cross-references: EMBL: X63539; NID: g44686; PIDN: CAA45102.1; PID: g581383
A; Cross-references: EMBL: X63539; NID: g44686; PIDN: CAA45102.1; PID: g581383
A; Note: sequence extracted from NCBI backbone (NCBIN:109731, NCBIP:109732)
B; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Peltwell, T.; Gentles, S.; Hamlin, N.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
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                                    C; Keywords: GTP binding; nucleotide binding; P-loop F;13-139/Domain: translation elongation factor Tu homology <ETU>F;19-26/Region: nucleotide-binding motif A (P-loop) F;136-139/Region: GTP-binding NKXD motif
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90.5%; Pred. No. 2.1e-08;
iive 0; Mismatches 2;
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Pred. No. 2.1e-08;
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90.5%;
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Best Local Similarity
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Best Local S:
Matches 19
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A; Reference number: A71630; MUID:99039499
A; Accession: C71672
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-394 < AND>
A; Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15101.1; PID:g386126
A; Experimental source: strain Madrid E
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Genetics:
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolc
C; Keywords: GTP binding; nucleotide binding; P-100p
F; 1397Domain: translation elongation factor Tu homology < ETU>
F; 136-1397Region: GTP-binding NKXD motif
F; 136-1397Region: GTP-binding SAK/L motif
F; 25, 26, 62, 136, 137, 139, 174 / Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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A;Molecule type: DNA
A;Residues: 1-394 <KANA
CCASIGUES: 1-394 <KANA
A;Residues: 1-394 <KANA
A;Residues: 1-394 <KANA
A;Residues: 1-394 <KANA
A;Residues: 1-394 <KANA
B;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a a
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C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 02-Feb-2001
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C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 02-Feb-2001
C;Accession: S62726; F82879
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten,
Nature 396, 133-140, 1998
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Score 107; DB 2; L
Pred. No. 1.5e-08;
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Pred. No. 2.1e-08;
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A;Reference number: S62726
A;Accession: S62726
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                                    87.0%;
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90.5%;
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                                Query Match 87.0
Best Local Similarity 90.5
Matches 19; Conservative
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A; Reference number: A82870
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Best Local Similarity
Matches 19; Conserv
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A; Residues: 1-394 <GLA>
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Gorgation factor EF-Tu [imported] - Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Saccession: G87143
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R; Cole, S.T.; Eiglmeier, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A; Hutherford, K.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A; Atitle: Massive gene decay in the leprosy bacillus.
A; Reference number: A86909; MuID:21128732; PMID:11234002
A; Recession: G87143
A; Molecule type: DNA
A; Residues: 1-396 <STO>
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
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Pred. No. 2.1e-08;
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1.397 <STO>
A,Cross references: GB:AE004843; GI
A,Experimental source: strain PAO1
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A;Gene: tufB; PA4277; tufA; PA4265
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90.5%;
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Best Local Similarity 85.7'
Matches 18; Conservative
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Matches 19; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-397 <ST2>
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G; Mycobacterium leprae
Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Mycobacies: Mycobacterium leprae elongation factor (EF-Tu) gene.
C; Mycobacterium leprae
C; Myc
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A; Molecule type: DNA
A; Residues: 'V', Z-128, 'GVPXILVA', 137, 'NKSDAVDDEELLE', 151, 'V', 153-280, 'L', 282-348, 'G', 35C
A; Residues: 'V', Z-128, 'GVPXILVA', 137, 'NKSDAVDDEELLE', 151, 'V', 153-280, 'L', 282-348, 'G', 35C
A; Cross-references: DDBJ:D13869
C; Genetics:
A; Genetics:
A; Genetics:
C; Genetics:

A; Gene: tuf
S; Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
C; Superfamily: translation elongation factor Tu; translation biosynthesis
E; 13-141/Domain: translation elongation factor Tu homology <ETU>
F; 19-26/Feglon: uncleotide-binding motif A (P-loop)
F; 138-141/Feglon: GTP-binding NXXD motif
F; 138-117/Region: GTP-binding SAK/L motif
F; 175-177/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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A; Residues: 1-128, GyPFILVALNKSDAVDDEELLELV', 153-280, 'L', 282-348,'G', 350-396 <SIL>
A; Residues: 1-128, GyPFILVALNKSDAVDDEELLELV', 153-280, 'L', 282-348,'G', 350-396 <SIL>
A; Cross-references: EMBL: 13276, NID:9293241; PIDN: AAA71969.1; PID:9293242
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1993
B; Dhandayuthapani, S.; Banu, M.J.; Kashiwabara, Y.
B; Blochem. 115, 664-669, 1994
A; Title: Cloning and sequence determination of the gene coding for the elongation factor A; Reference number: JC2262; MUID:94375410
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Pred. No. 2.1e-08;
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90.5%; Pred. No. 2.1e-08;
tive 0; Mismatches 2;
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llarity 90.5%;
Conservative
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Best Local Similarity 90.5
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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Length 396;

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A,Title: Complete genome seguence of Pseudomonas aeruginosa PA01, an opportunistic pa A,Reference number: A82950; MUID:20437337
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A.; Larbig,
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elongation factor Tu PA4277 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                              C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Nov-2000
C;Accession: F81111; C83111; C8311; C83111; C83111; C83111; C83111; C83111; C83111; C83111; C831
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85.7%; Pred. No. 2.1e-08;
Live 1; Mismatches 2; Indels
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translation elongation factor EF-Tu - Streptococcus oralis

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C. Accession: D95173

R. Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A.; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Accession: D95173
A; Status: preblamary
A; Molecule type: DNA
A; Residues: 1-398 KUR>
A; Residues: 1-398 KUR>
A; Experimental source: strain TIGR4
C; Genetics: A; Genetics: Sp1489
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolc
                                                                                                         Riudwig, W.; Welzeneger, M.; Betzl, D.; Leidel, E.; Lenz, T.; Ludvigsen, A.; Moellenhond, W.; Welzeneger, M.; Betzl, D.; Leidel, E.; Lenz, T.; Ludvigsen, A.; Moellenhond. 153, 241-247, 1990
ArTitle: Complete nucleotide sequences of seven eubacterial genes coding for the elongat A; Mitches nucleotide sequences of seven eubacterial genes coding for the elongat A; Maccession: F60663; MUD:90240875
A.Accession: F60663 MUD:90240875
A.Status: not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 1-398 <LUD>
A.Residues: 1-398 <LUD>
A.Residues: 1-398 <LUD>
A.Status: Translation elongation factor Tu; translation elongation factor Tu homology (S.Superfamily: translation elongation factor Tu homology (ETU)
B.;13-142/Domain: translation elongation factor Tu homology (ETU)
B.;13-142/Region: GTP-binding MXXD motif
B.;17-179/Region: GTP-binding SAK/L motif
B.;17-179/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
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C;Species: Streptococcus oralis
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 02-Feb-2001
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Best Local Similarity 85.7
Matches 18; Conservative
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/cgn2_6/ptcdata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/PcTu5_COMB.pep:* 4.5 Compugen Ltd hits satisfying chosen parameters: 231628 segs, 24425594 residues GenCore version Copyright (c) 1993 - 2000 SUMMARIES ٠. Minimum Match 0% Maximum Match 100% Listing first 100 summaries protein search, using sw model 2002, 07:43:01 123 1 MKEKFNRTKPHVNIGTIGHVDH BLOSUM62 Gapop 10.0 , Gapext Issued_Patents_AA:* length: 0 length: 2000000000 US-09-488-737-1 DB 620 1142 1148 Length August 22, Query Match Post-processing: oţ sed Title: Perfect score: Score Scoring table: ı Potal number 08 08 protein Sequence: Searched: Database Minimum Maximum ö Result No. Run ŏ

33, Appl 2, Appli 5, Appli တ်ဆဲဆဲ Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 2, Sequence 3, Sequence 2, Sequence 3, Sequence 2, Sequence 3, Sequence 2, Sequence 3, Sequence 5, Sequence 6, Sequen Sednence Sed US-08-626-994A-3
US-08-626-994A-3
US-08-957-742-1
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US-09-039-609-4
US-09-131-6481-16
US-09-131-6481-16
US-09-131-6481-16
US-09-131-6481-16
US-09-131-6481-16
US-08-989-370-5
US-08-989-370-5
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US-08-989-941B-39
US-08-989-941B-31
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US-08-989-941B-31
US-08-989-941B-31
US-08-989-941B-31
US-08-999-941B-31
US-08-999-941B PCT-US92-08012-2 US-08-889-841B-44 US-07-772-032-2 US-09-157-077-9 519 865 887 915 915 1264 1264 **თთთთთთთთთთთთ** 40.5 $\begin{array}{c} \mathbf{n} \, \mathbf{$ us-09-488-737-1.rai

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Sequence 6, Application US/09140466

Sequence 6, Application US/09140466

Sequence 6, Application US/09140466

Sequence 6, Application US/09140466

SERREAL INFORMATION:

APPLICANT: CLOUGH, BARBARA

APPLICANT: WILSON, ROBERT

TITLE OF INVENTION: AN EFT TU PROTEIN ENCODED ON THE PLASTID DNA OF THE

TITLE OF INVENTION: AN EFT TO PROTEIN SYNTHESIS INHIBITORS

TITLE OF INVENTION: BFRECTIVE AS ANTI-MALARIAL COMPOUNDS

FILE REPRESENCE: N68837B GCW PJC DP

CURRENT APPLICATION NUMBER: US/09/140,466

CURRENT FILING DATE: 1999-08-28

EARLIER PILING DATE: 1999-08-28

SERLIER PILING DATE: 1999-08-28

NUMBER OF SED ID NOS: 14

SEQ ID NO 6

SEQ ID NO 6

LENGTH. 204
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Patent No. 6266160

GENERAL INFORMATION:
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
TITLE OF INVENTION: AN ER-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: BALEATIA AND PROTEIN SYNTHESIS INHIBITORS
CURRENT APPLICATION NUMBER: US/09/140,466
CURRENT APPLICATION NUMBER: US/09/140,466
EARLIER PELICATION NUMBER: US/09/140,466
BARLIER FILING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NOS: 14
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Pred. No. 1.1e-08;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 111; DB 4;
Pred. No. 3.9e-10;
1; Mismatches 1;
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90.5%;
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81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-140-466-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.9
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Cryptomonas phi
US-09-140-466-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 408
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3 RDKFERSKPHVNIGTIGHVDH 23

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                                                                     APPLICANT: CLOUGH, BARBARA
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: WILSON, ROBERT
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: ALEREA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REFERENCE: NG8837B GGW PJC DP
CURRENT APPLICATION NUMBER: US/09/140,466
CURRENT FILING DATE: 1998-08-26
EARLIER PELLING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLOUGH, BARBARA
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: WILSON, ROBERT
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REPERENCE: N68837B GCW DJC DP
CURRENT APPLICATION NUMBER: US/09/140,466
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: US 60/056,246
EARLIER FILING DATE: 1997-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.5%; Score 99; DB 4; Length 409
81.0%; Pred. No. 3.4e-08;
Live 1; Mismatches 3; Indels
; Sequence 3, Application US/09140466
; Patent No. 6268160
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09140466
; Patent No. 6268160
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/09140466 ; Patent No. 6268160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Cyanophora paradoxa
US-09-140-466-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Anacystis nidulans
US-09-140-466-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.5
Best Local Similarity 81.0
Matches 17; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 409
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US-09-140-466-2
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
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APPLICANT: Fisher, Paul B.
APPLICANT: Fisher, Paul B.
APPLICANT: Shen, Ruoqian
TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND
TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED
TITLE OF INVENTION: MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                Length 462;
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                                                                                                      ; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 462 US-08-299-351-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,377
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 2;
Pred. No. 1.9;
2; Mismatches
                                                                                                                                                                                             Score 51; DB 1;
Pred. No. 1.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/37590-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
STRENDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/08371377; Patent No. 5851764; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: not relevant not relevant
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                                                                                                                                                                                             41.5%;
60.0%;
J. Biol. Chem.
264
                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                        7 RTKPHVNIGTIGHVD 21
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3 KEKTHINIVVIGHVD 17
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                                                           5791-5798
1989
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-08-371-377-18
                                                             PAGES:
                                                                                   DATE:
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Sequence 1, Application US/0829351

Sequence 1, Application US-0829

TITLE OF INVENTION: RHEDMAYDLOIGICAL DISEASES BY DETECTION OF ANTI-EF-laipha TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: HOVEY, WILLIAMS, TIMMONS & COLLINS

STREET: Missouri

COUNTRY: Kanaas City

STATE: Missouri

COUNTRY: USA

ZIP: 64106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
         APPLICANT: CLOUGH, BARBARA
APPLICANT: PEDEISER, PEDEER
APPLICANT: PEDEISER, PEDEER
APPLICANT: WILSON, ROBERT
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
TITLE OF INVENTION: EPEECTIVE AS ANTI-MALARIAL COMPOUNDS
TITLE OF INVENTION: EPEECTIVE AS ANTI-MALARIAL COMPOUNDS
TITLE OF INVENTION: BOX 09.70 by COURERY APPLICATION NUMBER: US/09/140,466
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: US 60/056,246
EARLIER PILING DATE: 1997-08-28
NUMBER OF SEO ID NOS: 14
SOFTWARE: PATENTIN VOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB 4; Length 410
Pred. No. 7.9e-05;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,351
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CLEVELAND JUBER: 36106
REGISTRATION NUMBER: 36106
REFERENCE/POCKET NUMBER: 2270
TELECOMMUNICATION INFORMATION:
TELEFAM: (816) 474-9050
TELEFAM: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT CRGANISM: Plasmodium falciparum US-09-140-466-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.4%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 462 amino acids amino acid
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 410
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Sequence 19, Application US/08454439

Patent No. 5591618

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE MAISHALL, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois
                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB
Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAX-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
                                                                                                                                                             CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY AGENT INFORMATION:
NAME: NO. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: 08/123,932
17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
77, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-221-817-19
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Patent No. 6265185

GENERAL INFORMATION:
APPLICANT: Muller, Sven
APPLICANT: Dalbage, Henrik
TITLE OF INVENTION: No. 6265185el Yeast Promoters Sultable For Expres
TITLE OF INVENTION: No. 6265185el Yeast Promoters Sultable For Expres
TITLE OF INVENTION: Heterologous Expression of Proteins in Yeast
FILE REFERENCE: 4791.204-US
CURRENT FILING DATE: 1998-10-19
EARLIER FILING DATE: 1998-10-19
EARLIER FILING DATE: 1996-05-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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1.9;
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Pred. No. 2.8;
PATENT NO. 5225348

PAPLICANT: HAGATA, SHIGEKAZU; SUGANO, SUMIO; KIM, DONG W.;
JUTSUKI, TAICHI; KAZIRO, YOSHITO
TITLE OF INVENTION: DNA FRAGMENT AND EXPRESSION PLASMID
CONTAINING THE DNA FRAGMENT
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION BDAT:
APPLICATION NUMBER: US/07/447,823
FILING DATE: 08-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                        Score 51;
Pred. No.
                                                                                                                                                                                                                                                      41.5%;
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60.08;
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.7
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                           7 RTKPHVNIGTIGHVD 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 RTKPHVNIGTIGHVD 21
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Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: EF-lalpha
US-09-174-768-4
                                                                                                                                                                                 LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-174-768-4
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                                                                                                                                                               SEQ ID NO:1:
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chanty, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor TITLE OF INVENTION: Rinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 6.3;
6; Mismatches 3; Indels
                                                                                         DB 5; Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
CITY: 111inois
COUNTRY: USA
21P: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Fleppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                         Score 49; DB 5
Pred. No. 6.3;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NOTE:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 18, Application US/08454439
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43.8%;
                                                                                         39.8%;
43.8%;
                                                                    Query Match
Best Local Similarity 43.8°
Conservative
                                                                                                                                                                                                          342 FSKKKPHASVGTHGYM 357
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Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                                                                                                              5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-221-817-18
protein
; MOLECULE TYPE:
PCT-US94-10487-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-454-439-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application PC/TUS9410487
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun ADDRESSEE: Borun ADDRESSEE: Borun CITY: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA 21P: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60606

ZIP: 60606

MEDIUM TYREADABLE FORM:
MEDIUM TYRE IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 1
Pred. No. 6.3;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
         ATTORNEY/AGENT INFORMATION:
NAME: NO. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/CACKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUBBER: 08/221,817
FILING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.8%;
Best Local Similarity 43.8%;
Matches 7; Conservative
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| 342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-454-439-19
                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
  CLASSIFICATION:
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PCT-US94-10487-19
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5 FNRTKPHVNIGTIGHV 20
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MOLECULE TYPE: protein
PCT-US94-10487-18
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US-08-221-817-20
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                                 APPLICANT: Chantry, David
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hockstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
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Sequence 18, Application PC/TUS9410487

GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                   COMPUTER: DEPOPM disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STAME: Llinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB Pred. No. 6.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NO. 5531618and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/CDOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: 2132) 474-6300
TELEE: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 689 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.8%;
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Best Local Similarity 43.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
                   GENERAL INFORMATION:
Patent No. 5591618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Patent No. 5332151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor; TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor; NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 17 SEP 1993
CLASSIFICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
NAME: NOLAND, GREAR E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
RELECHONE: (312) 474-6300:
TELECHONE: (312) 474-6300:
TELECHONE: (312) 474-6300:
TELECHONE: (312) 474-6448
TELECHONE: (312) 474-648
TELECHONE: (312) 474-648
TELECHONE: (312) 474-648
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 689 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 43.8
Matches 7; Conservative
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application PC/TUS9410487
Sequence 20, Application PC/TUS9410487
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 699;
                                                                                                                                                                Score 49; DB 1; Length 699;
Pred. No. 6.4;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.8%; Score 49; DB 5
43.8%; Pred. No. 6.4;
Live 6; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,817
FILING DATE: 31 MAR 1994
CLASSIFICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
ATTORWEY/AGENT INFORMATION:
ATTORWEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/3:
TELECHOMONICATION INFORMATION:
TELECHOMONICATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
                                                                                                                                                                Query Match 39.8%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                           |:: ||| ::|| |::
343 FSKKKPHASVGTHGYM 358
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                                  MOLECULE TYPE: protein US-08-454-439-20
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 18
PCT-US94-10487-20
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Sequence 20, Application US/08454439

Batent No. 5591618

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: A No. 5591618e1 G Protein-Coupled Receptor TITLE OF INVENTION: Kinase GRK6

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
SSRREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 1; Length 699;
Pred. No. 6.4;
6; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION NUMBER: US 08/221,817
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/123,932
FILING DATE: TEP 1993
APPLICATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
RELEPAN: (312) 474-6300
TELEPAN: (312) 474-6300
TELEPAN: (312) 474-6300
TELEPAN: (312) 474-6300
TELEPAN: (500 mains of the content of the conte
                        ATTORNEY AGENT INFORMATION:
NAME: NO. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: almino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.8%;
Best Local Similarity 43.8%;
Matches 7; Conservative (
   FILING DATE: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 699 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:: ||| ::|| |::
343 FSKKKPHASVGTHGYM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-221-817-20
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WESULT 21
US-09-273-565-40

Sequence 40. Application US/09273565A

Patent No. 6166190

GENERAL INFORMATION:
PAPLICANT: WATANABE, TAKESHI

APPLICANT: WATANABE, TAKESHI

CURRENT PAPLICATION SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME

FILE REFERENCE: 0-53599

CURRENT PAPLICATION NUMBER: US/09/273,565A

CURRENT PAPLICATION NUMBER: 09/055,699

EARLIER FILING DATE: 1999-03-19

EARLIER FILING DATE: 1997-03-19

EARLIER FILING DATE: 1997-03-19

EARLIER FILING DATE: 1997-03-05

SOFTWARE: PAPENTIN VOINBER: JP 69163/1997

EARLIER FILING DATE: 1997-03-05

NUMBER OF SEQ ID NOS: 95

SOFTWARE: PATENTIN VOINBER: 2.1

SEQ ID NO 40

LENGTH: 499
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                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 3
Pred. No. 6.3;
1; Mismatches
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Pred. No. 6.3;
1; Mismatches
APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %209-565-538-40
%Sequence 40, Application US/09565538
%Patent No. 6333404
%PRINTENT INFORMATION:
%APPLICANT: FUJIWARA, TSUTOMU
                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,170
                                                                                         FILING DATE:
TELECOMBUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELERAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                              39.0%;
69.2%;
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69.2%;
                                                                                                                                                                                                                                       LENGTH: 499 amino acids TYPE: amino acid
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Best Local Similarity 69.2%
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                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-055-699-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 KPHVNIGTIGHVD 21
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72 KEHVNVVFIGHVD 84
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US-09-273-565-40
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72 KEHVNVVFIGHVD 84
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Best Local Similarity
Matches 9; Conserva
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                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pennsylvania Avenue, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Subtrue, Mion, Zinn, Macpeak & Seas SABEET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,170A
        US-08-20-170A-40

Sequence 40, Application US/08820170A

Patent No. 5831058

GENERAL INFORMATION:
APPLICANT: Takeshi, WATANABE
APPLICANT: Takeshi, WATANABE
APPLICANT: TOYOMASA, HORIE
TITLE OF INVENTION: HUMAN GENE
TITLE OF INVENTION: HUMAN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/09055699; Patent No. 6005088; GENERAL INFORMATION: APPLICANT: TSULOMU, FUJIWARA APPLICANT: Takeshi, WATANABE APPLICANT: Toyomasa, KATAGIRI TITLE OF INVENTION: HUMAN GENE NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C. COUNTRY: United States ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-820-170A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 KPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |||: |||||
72 KEHVNVVFIGHVD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
US-09-055-699-40
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Gaps
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Sequence 12, Application PC/TUS9508565

Sequence 12, Application: Anthony R.

APPLICANT: Cashmore, Anthony R.

APPLICANT: Ahmad, Margaret

APPLICANT: Lin, Chentae

TITLE OF INVENTION: Blue Light Photoreceptors and Methods of

TITLE OF INVENTION: Using the Same

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris

STREET: One Liberty Place, 46th floor

CITY: Philadiphia

STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 18;
3; Mismatches 6; Indels
                                                                                                            Length 480;
                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08565
                                                                                                        Score 45; DB 2;
Pred. No. 18;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,255
FILING DATE: 08-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEATY Ph.D., Kathryn
REFERENCE/DOCKET NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
TELECPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
"""""" amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
US-09-442-100-11
; Sequence 11, Application US/09442100
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47.1%;
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237 EEPTSRLSPHLKFGTIG 253
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Best Local Similarity 4/...
8; Conservative
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                                                                                                            Query Match
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                2 KEKFNRTKPHVNIGTIG 18
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       ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-272-255-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   single
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                            PCT-US95-08565-12
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; Sequence 12, Application US/08272255
; Patent No. 5824859;
GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R.
APPLICANT: Almad, Margaret
APPLICANT: Almad, Margaret
APPLICANT: Lin, Chentan
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STRATE: PA
COUNTY: USA
ZIP: 19103
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 6.3;
1; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/272,255
FILING DATE: 08-JUL-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UPN-1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENTINFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.0%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 480 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.0
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-565-538-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 KPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 499
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Gaps

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Sequence 90, Application US/09106075A

Patent No. 6316250

Sequence 90, Application US/09106075A

Patent No. 6316250

GENERAL INFORMATION:

APPLICANT: Hjelle MD, Brian

APPLICANT: Jenison, Steve

TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of

TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of

TITLE OF INVENTION: Hjelle et al. (210312.0009)

FILE REFERENCE: 10312-801, Hjelle et al. (210312.0009)

CURRENT APPLICATION NUMBER: US/09/106,075A

CURRENT FILING DATE: 1994-03-22

PRIOR FILING DATE: 1994-03-22

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-09-13

PRIOR FILING DATE: 1993-08-25

NUMBER OF SEQ ID NOS: 90

SEOTTANES PATENTIN VET. 2.1
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                                                                                                                                                                                                                                               Length 1142;
                                                                                                                                                                                                                                                 Score 42; DB 4; Length 114
Pred. No. 1.5e+02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GICNAC '2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE SACS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
CITY: Reston
STATE: U.S.A.
    08/111,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/08626994A; Patent No. 5798244
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1993-08-25
NUMBER OF SEQ ID NOS: 90
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 89
                                                                                                                                                                                                                                                 34.1%;
36.8%;
                                                                                                                                   TYPE: PRT; ORGANISM: Prospect Hill virus
US-09-106-075A-89
                                                                                                                                                                                                                                                                                                                                                                30 OSFNITEPHITSNSLEWD 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             934 QSFNVTEPHISTSALEWID 952
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                                                                                                                                                                                                                                                 Query Match 34.1
Best Local Similarity 36.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Puumala virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 90
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APPLICANT: Hjelle MD, Brian
APPLICANT: Hjelle MD, Steve
APPLICANT: Jenison, Steve
TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of
TITLE OF INVENTION: the HARDS Virus.
TITLE REFERENCE: 10312-801, Hjelle et al. (210312.0009)
CURRENT APPLICATION NUMBER: US/09/106,075A
CURRENT FILING DATE: 1998-06-29
PRIOR PILING DATE: 1994-03-22
PRIOR PILING DATE: 1993-09-18
PRIOR FILING DATE: 1993-09-18
PRIOR FILING DATE: 1993-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                    APPLICANT: Xu, Tian
APPLICANT: Tao, Wufan
APPLICANT: Tao, Weiyi
APPLICANT: Wang, Weiyi
APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 620; 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
CMPUTER READABLE FORM:
MEDIUM TYPE Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy STEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 74;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATOCNEY/CENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-003
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 790-9990
TELEFAX: (6111 PENNIE
INFORMATION FOR SEQ ID 0: 11:
                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 89, Application US/09106075A Patent No. 6316250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.1%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 620 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-442-100-11
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 NRTKPHVNIGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :||:|:||
3 NTNRPHLNLGT 13
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
                    INFORMATION
Patent No. 6359193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-106-075A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                            33.3%; Score 41; DB 3; Length 339;
40.0%; Pred. No. 54;
tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC '2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.3%; Score 41; DB 40.0%; Pred. No. 59; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: 1BM PC compatible
OPPERATING SYSTEM: MS-DOS
COMPUTER: WORD PC compatible
OPPERATING SYSTEM: MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,994A
FILING DATE: April 3, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY AGENT INFORMATION:
NAME: ATOOLD TURK
REGISTRATION NUMBER: P14595
TELECOMMUNICATION INFORMATION:
TELECOMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08626994A Patent No. 5798244
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |: || | || : | |:
96 KNFSLTKSSVRIGQLMHYDY 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 EKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 40.09
Matches 8; Conservative
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Best Local Similarity 40.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1941 Rola CITY: Reston STATE: Virginia COUNTRY: U.S.A. ZIP: 20191
                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-957-742-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
US-08-626-994A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ouery Match 33.3%; Score 41; DB 1; Length 339; Best Local Similarity 40.0%; Pred. No. 54; Matches 8; Conservative 4; Mismatches 0 - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-957-742-3
Sequence 3, Application US/08957742
Sequence 1017743
GENERAL INFORMATION:
APPLICANT: SAULCHI TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC 2,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Greenblum & Bernstein, P.L.C. STREET: 1941 Roland Clarke Place CTTY: Reston STATE: Virginia COUNTRY: U.S.A.
         COMPUTER READBLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: 1.44 diskette
COMPUTER: 1.14 mortalible
COMPUTER: 1.10 DATA:
APPLICATION DATA:
APPLICATION NUMBER: 37 1995
ATONNEY, ARGNIT 1180, 1995
ATONNEY, ARGNIT 1180, 1995
ATONNEY, ARGNIT 1180
TELEPHONE: (703) 716-1191
TELEPHONE: (703) 716-1191
TELEPHONE: (703) 716-1191
TELEPHONE: CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRER: 18/626,994
FILING DATE: APT11 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: APT11 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARDOID TURK
REGISTATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EKFNRTKPHVNIGTIGHVDH 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20191
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APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22040-0747
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40.5; DE
Pred. No. 62;
5; Mismatches
                                                                                                                    FILING DATE: 16 MAR-198
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,623
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70275
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1488-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08646981; Patent No. 5852183; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||: :| || |: |||
279 VKEELPQERPAVN-QTVAEVDH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,181
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NAME: WEINER, WARC S
REGISTRATION NUMBER: 32,1
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 16
                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-646-981-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-039-609-4
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59;
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                                     Sequence 1, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC '2,8-TITLE OF INVENTION: SIA'ZITRANSFERASE
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
US-09-039-609-4
; Sequence 4, Application US/09039609
; Patent No. 610743;
GENERAL INFORMATION:
APPLICANT: ALBONE, EARL
APPLICANT: RIKLY, KRISTINE
TITLE OF INVENTION: A KRINGLE-RELATED CLONE,
INTILE OF INVENTION: A THEB247
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Rather & Prestia
STREET: P.O. BOX 980
CITY: Valley Forge
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke place
CITY: Reston
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%; Score 41; DB
40.0%; Pred. No. 59;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435 /
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAME: Arnold Turk

REGISTRATION NUMBER: 33,094

REFERENCE/DOCKET NUMBER: P14595

FELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 716-1191

TELEPRAX: (703) 716-1191

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

TYPE: amino acid

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

GS-08-957-742-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 KNFSLTKSSVRIGQLMHYDY 115
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Best Local Similarity 40.0v
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COMPUTER READABLE FORM:
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                   .08-957-742-1
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Gaps

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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 96;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 407; 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989;370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 3
Pred. No. 96;
3; Mismatches
                                                     ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.404C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-490
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-DEC-1997
CLASSIFICATION:
ATONNEY/GENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.404C5
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
APPLICATION NUMBER: US/08/989,370 FILING DATE: 12-DEC-1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMBER: US/08/989;370
12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08989370 Patent No. 6013268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%;
38.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || || || 1
146 QKLQAEAPHIVVGTPGRV 163
                                                                                                                                                                                                                               LENGTH: 407 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EKFNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EKFNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.59
Best Local Similarity 38.99
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                              Query Match 32.5
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 Columic CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104-7092
                                                                                                                                                                                                                                                                                        linear
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US-08-989-370-5
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US-08-993-370-5
Sequence 5, Application US/08989370
Fatent No. 6013268
GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                          Length 334;
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Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
CURRENT FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                        32.5%; Score 40; DB 2; 45.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                            US-09-131-648-1
; Sequence 1, Application US/09131648
; Patent No. 6168220
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       178 EEQFNGTYRVVSVLPIGHQD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.5%;
50.0%;
                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVD 21
                   LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                Ouery Match
Best Local Similarity 45.09
Watches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: 2635136
US-09-131-648-1
                                                     SSS: single
linear
   SEQUENCE CHARACTERISTICS
                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-646-981-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|: ||||| |:
99 RFHTTKPHVICNTL 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 7; Conserv
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LENGTH: 336
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                                                                                                                                                                                           Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 4; Length 508; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KIENY, Marie-Paule
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: MOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: gp160 VARIANT
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
COUNTRY: Uniqinia
COUNTRY: Uniqinia
COUNTRY: Uniqinia
ZIP: 22313-1404
                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BW PC compatible
COMPUTER: TBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,240A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PROR APPLICATION 1995
FILING DATE: 31-DEC-1992
ATTONEY/AGENT INFORMATION:
ANNUMBER: 31-DEC-1992
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                           Score 40; DB 3; 1
Pred. No. 1.1e+02;
3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 474
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Teskin, Robin L.
RECISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUBBER: 017753-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: August 22, 2002, 07:44:32
                                                                                                                                                                                                                                                                                                                                                                                                    US-08-472-240A-16; Sequence 16, Application US/08472240A; Patent No. 6284248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 508 amino acids
amino acid
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                       :||| | |: |:
186 KKFNGTGPCTNVSTV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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232 KKFNGTGPCTNVSTV 246
                                                                                                                                                                                                                                                                               3 EKFNRTKPHVNIGTI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-472-240A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EKFNRTKPHVNIGTI 17
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Best Local Similarity
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                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                       ) ORGANISM: HIV
US-08-889-841B-39
                                                                                                                                                                                                                                                                                                                      q
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                                                                          RESULT 37
US-08-889-841B-46
; Sequence 46, Application US/08889841B
; Sequence 46, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: -14918-703C1P
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FESSEEQ for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-00-889-841B-36

Sequence 36, Application US/08889841B

GENERAL INFORMATION:
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B

CURRENT FILING DATE: 1997-07-08

PRIOR PILING DATE: 1997-07-08

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FESSESQ for Windows Version 3.0

SEQ ID NO 36

LENGTH: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 3; Length 455;
Pred. No. 1.1e+02;
3; Mismatches 5; Indels
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TITLE OF INVERVED HIS WOVELOPE POLYPEPTIDES AND VACCINE
TILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
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MS-08-889-841B-39
: Sequence 39, Application US/08889841B
; GENERAL INFORMATION:
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46.78;
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Best Local Similarity 46.7%;
Matches 7; Conservative
  Query Match 32.5
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Matches 7; Conservative
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189 KKFNGTGPCTNVSTV 203
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US-08-889-841B-46
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Compugen Ltd
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         GenCore version Copyright (c) 1993 - 2000
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Listing first 100 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Helicobacter pylori membrane proteins - and related polypeptide(s) and antibodies, useful for active or passive immunisation and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane protein; vaccine; immunisation; immunoassay;
diagnostic; affinity purification; gastritis; peptic ulcer;
gastric cancer.
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22 AA
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AAW33404;
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 Length
                                      Indels
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(INNR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
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100.0%; Score 123; DB 18; 100.0%; Pred. No. 4.9e-13;
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100.0%; Pred. No. 4.9e-13;
tive 0; Mismatches 0;
                                      Mismatches
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97US-0831310.
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01-APR-1997;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aucres, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also used in the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen corrections of the monitogous nucleic acids sequence is also useful to screen corrections and to obtain antibodia acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic from a directly from WIPO at the wipo.int/pub/published_pct_sequences.
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Pred. No. 7.7e-11;
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                     Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611495/70.
N-PSDB; AAS53681.
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Matches 21; Conserv
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                    WO200170955-A2.
                                                                                                                                                                                              26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
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AAB15890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of a 50 kDa Helicobacter pylori polypeptide designated GHPO 750. It was deduced from an isolated genomic DNA sequence (see AAV07963). The invention provides a family of 76 kDa Helicobacter polypeptides (see AAW73022-32), as well as GHPO 750 and a 32 kDa polypeptides (see AAW73034), and also polynucleotides (see AAV72001, AAV073012-21 and AAV07963-64) encoding them, expression cassettes, and methods for producting the unprocessed mature polypeptides in host cells. The polypeptides can be used in waccination methods to prevent or treat Hb Infection in a mammal. Methods and products of the invention allow treatment and prevention of gastroduodenal diseases associated with Hb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and ducdenal ulcers. Detection and diagnostic methods are also provided. GHPO 750 was demonstrated to be a protective antigen. Unlike the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        demonstrated to be a protective antigen. Unlike the other polypeptides of the invention, GHPO 750 is not a secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.9%; Score 118; DB 19; Length 399; 100.0%; Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                              Tomb J;
                                         GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          Al-Garawi A, Kleanthous H, Lissolo L, Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Helicobacter pylori 32 kDa polypeptide GHPO 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 150-152; 184pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori cellular
                                                                                                                                                                                                                                                                                        97US-0834666.
97US-0831310.
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                                                                                                          Helicobacter pylori
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tes 21, Conserv
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01-APR-1997;
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Sequence

Query Match

Matches

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AAU35822 RESULT

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Length 399;

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are care themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus auceus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The cinvention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in cay wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part form at directly from without at
                                                                                                                                                                  Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 394;
                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                  Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. coli cellular proliferation protein #419.
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1; Mismatches
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                                                                                                                                                                  Zyskind JW,
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                   23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
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                                                                                                                                                                  Ohlsen KL,
                                                                                                                           (ELIT-) ELITRA PHARM INC.
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N-PSDB; AAS52628.
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nes 19; Conserv
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                                                                                                                                                                  Haselbeck R,
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                                                                                                                                                                                                                                                   Carr GJ;
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                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
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                                                                                                                                                                                                                                                 Ohlsen KL, Trawick J, Forsyth RA, Froelich JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 177-178; 316pp; English.
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                                                                                                                       27-JAN-2000; 2000WO-US02200
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23-MAY-2000; 2000US-206848P.
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hes 19; Conservative
                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC
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Escherichia coli.
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Matches 199
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AAU34769

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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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Pred. No. 1e-09;
1; Mismatches
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ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                Ohlsen KL, Zyskind JW,
Xu HH;
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2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                2000US-253625P.
2000US-257931P.
2001US-269308P.
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llarity 90.5%;
Conservative
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                                                                                                                                                                       (ELIT-) ELITRA PHARM INC
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Best Local Similarity
Matches 19; Conserv
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                                      26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                         Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae cellular proliferation protein #107.
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antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Seq ID No 10431; 511pp; English.
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                                        2000US-24257BP.
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2001US-269308P.
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Matches 19; Conserv
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27-NOV-2000;
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                      26-MAY-2000;
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Trawick JD,

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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at they wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Riebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
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2000US-207727P.
2000US-242578P.
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2000US-257931P.
21-MAR-2001; 2001WO-US09180.
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Xu HH;
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Matches 19; Conservative
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N-PSDB; AAS56230.
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Yamamoto RT,
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22-DEC-2000;
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                                                                21-MAR-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wile wile and the printed specification, but was obtained in electronic fitp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 90.59
Matches 19; Conservative
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Yamamoto RT,
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Length 409;

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella comenuoniae, Pseudomonas aeruginosa and Enterococcus facerils. The Escherichia is also useful for the identification of potential new targets invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used in proliferation, to the expressed proteins. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Contract directly from MIPO at this patent did not form part
                                                                                                                             Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 106, DB 22; Length 397;
Pred. No. 6.7e-09;
1; Mismatches 2; Indels
                                                                                                                             Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa cellular proliferation protein #399.
                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                             Wall D,
                                                                                                                                                                                                                                                                                                                Example 3; Seq ID No 11995; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                             Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU36409 standard; Protein; 397 AA.
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                             Ohlsen KL,
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                                                                                                                             Haselbeck R,
                                                                                                                                                (amamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteriu are useful for producing amino acids, nucleic acids, vitemins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                      mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                          Hayashi M, Ochiai K, Yokoi H;
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                                                                                                                                                                                                                                                                                                                                                                                                                        claim 29; SEQ ID NO: 6937; 246pp + Sequence Listing; English.
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Pred. No. 6.6e-09;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa cellular proliferation protein #392.
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                                                                                                                                                                                      Ando S, Hayası
da M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU36402 standard; Protein; 397 AA.
                                                                                                                                                                                                              Ikeda M,
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90.5%;
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2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                           99JP-0377484.
2000JP-0159162.
2000JP-0280988.
                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK
                     18-DEC-2000; 2000EP-0127688
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                                                                                                                                                                                          Mizoguchi H,
Senoh A, Ike
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Best Local Similarity 90.5
Matches 19; Conservative
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23-MAY-2000;
26-MAY-2000;
23-0CT-2000;
                                                                                   -APR-2000;
                                                                                                       03-AUG-2000;
                                                                                                                                                                                        Nakagawa S,
Tateishi N,
                                                               16-DEC-1999;
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AAU36402;

RESULT 12 AAU36402

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen of in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part to the printed specification, but was obtained in electronic for the printed specification, but was obtained in electronic for the printed specification, but was obtained in electronic form part
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                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.2%; Score 106; DB 22;
85.7%; Pred. No. 6.7e-09;
tive 3; Mismatches 0;
                                                                                                                                                                                    Wall D,
                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Seq ID No 13171; 511pp; English.
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                                                                                                                                                                                    Zyskind JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 kekydrskphvnigtighvdh 23
                     2000US-242578P.
2000US-253625P.
2000US-257931P.
  2000US-207727P
                                                                                        2001US-269308P
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                                                                                                                                                                                    KL,
                                                                                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                  Ohlsen
                                                                                                                                                                                                                                                       WPI; 2001-611495/70.
N-PSDB; AAS55437.
                     23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                  Haselbeck R,
Yamamoto RT,
                                                                                        16-FEB-2001;
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Conter The sequence data for this patent did not form part for the printed specification, but was obtained in electronic form the property of the printed specification.
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                                                                                                                                                             Trawick JD, Carr GJ;
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85.7%; Pred. No. 6.7e-09;
iive 1; Mismatches 2;
                                                                                                                                                          Ohlsen KL, Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                Example 3; Seq ID No 12002; 511pp; English.
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                     2000US-253625P.
2000US-257931P.
2001US-269308P.
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2000US-242578P
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2000US-206848P.
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Best Local Similarity 85.79
Matches 18; Conservative
                                                                                                               (ELIT-) ELITRA PHARM INC
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                                                                                                                                                                                  Xu HH;
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                                                                                                                                                          Haselbeck R,
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23-MAY-2000;
                       27 - NOV - 2000;
                                          22-DEC-2000;
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microorganism. This protein also has the ability to catalyse the transfer of aminoacyl-tRNA to a ribosome A site, and has a molecular weight of about 45 kD as determined by SDS-PAGE. The primers used to isolate the DNA encoding this sequence can also be used to detect the EF-Tu gene. The primers are also used for the highly accurate detection of microorganisms of the genus Lactobacillus, by specifically detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the gene tuf into tuff encoding a protein, resistant to the elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tuff) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence of translation elongation factor Tul encoded by tufl gene.
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                                                                                                                                                    Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transform streptomycetes to resistant pheno-type
                                                                                                                                                     Score 103; DB 18;
Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102; DB 13;
Pred. No. 2.9e-08;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 1 and Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bosch L, Vijgenboom
                                                                                                                                                                                  Mismatches
                                                                                   the EF-Tu gene from these microorganisms.
                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                        AAR20242 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.9%;
81.0%;
                                                                                                                                                       83.7%;
85.7%;
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90EP-0201851.
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                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces ramocissimus.
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kerkman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-017874/03.
                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  elongation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ20215
                                                                                                              396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGM,
                                                                                                                                                                                                                                                                                                                                                               15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woudt LP;
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                     AAR20242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luiten
                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the elongation factor Tu (EF-Tu) of the invention. The DNA encoding this sequence was isolated from Lactobacillus paracasel subspecies paracasel using the primers shown in AAT92&20 and AAT92&21. This sequence is involved in the polypeptide chain elongation reaction in the blosynthesis of proteins in a Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tu; EF-Tu; Lactobacillus; polypeptide chain elongation;
is; aminoacyl-tRNA transfer; ribosome A site; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                      valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the gene tuf into tufR encoding a protein, resistant to the elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                          Substitution of residue 378 of the elongation factor (EF-Tu) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus polypeptide chain elongating factor Tu - used for detecting microorganisms belonging to the genus Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                             Length 396;
                                                          Heinstra
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                                                                                                                                          nseq
                                                                                                                                                                                                                                                                                                                                                             Score 105; DB 13;
Pred. No. 9.6e-09;
1; Mismatches 2;
                                                         Vijgenboom E,
                                                                                                                                                       transform streptomycetes to resistant pheno-type
                                                                                                                                          protein conferring resistance to elfamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactobacillus paracasei subspecies paracasei.
                                                                                                                                                                               Example; Pages 16-18; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW30303 standard; Protein; 396 AA.
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                                                         Bosch
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    90EP-0201851
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                              (KONN ) GIST-BROCADES NV
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protein biosynthesis;
                                                         Kerkman
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N-PSDB; AAT92619.
                                                                                              WPI; 1992-017874/03
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                      396 AA;
                                                                                                             N-PSDB; AAQ20216
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    10-JUL-1990;
                                                        Luiten RGM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-1997
                                                                                                                                                                                                                                                                                                                        Seguence
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                                                                       Woudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. Of elfamycin by actinomycetes is removed by mutating the gene tuf into tufR encoding a protein resistant to an elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elfamycin-resistant elingation factor EF-TuR Pro 378
                                                                                                                                                                                                                                                   Heinstra PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 13; Length 3
Pred. No. 2.9e-08;
2; Mismatches 2; Indels
   Elfamycin resistant actinomycetes; antibiotic resistant; elongation factor.
                                                                                                                                                                                                                                                                                                                                          New protein conferring resistance to elfamycin - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elfamycin resistant actinomycetes; antibiotic resistant;
                                                                                                                                                                                                                                              Kerkman R, Bosch L, Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                         transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR20247 standard; Protein; 396 AA.
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81.0%;
                                                                                                                                         91EP-0201702
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90EP-0201851
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90EP-0201851
                                                 Streptomyces ramocissimus.
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                                                                                                                                                                                                                   (KONN ) GIST-BROCADES NV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded by SrtufR1 gene
                                                                                                                                                                                                                                                                                            WPI; 1992-017874/03.
N-PSDB; AAQ20219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elongation factor
                                                                                                                                       02-JUL-1991;
                                                                                                                                                                      02-JUL-1991;
10-JUL-1990;
                                                                                                                                                                                                                                                 Luiten RGM,
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10-JUL-1990;
                                                                                                            15-JAN-1992
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Matches
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                                                                                                                                                                                    elfamycin-resistant elingation factor EF-TuR Val 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of elfamycin-resistant elingation factor EF-TuR Thr 378\, encoded by SrtufRl gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heinstra PW;
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                                                                                                                                                                                                                              Elfamycin resistant actinomycetes; antibiotic resistant;
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Pred. No. 2.9e-08;
}; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein conferring resistance to elfamycin
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                                                                                         AAR20245 standard; Protein; 396 AA.
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81.0%;
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                                                                                                                                                                                                 encoded by SrtufRl gene.
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 AA;
                                                                                                                                                                                                                                              elongation factor
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10-JUL-1990;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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the limiting factor for the prodn. of elfamycin by actinomycetes removed by mutating the gene tuf into tuff encoding a protein resistant to an elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
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                                                                                                                                                                                           Length 396;
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                                                                                                                                                                                           Query Match 82.9%; Score 102; DB 13; Best Local Similarity 81.0%; Pred. No. 2.9e-08; Matches 17; Conservative 2; Mismatches 2;
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99US-0128714.
99US-0129845.
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99US-0130510.
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99US-0134768
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99US-0135124
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99US-0135629
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99US-0136392
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                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH
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                                                                                                                         AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1999;
23-APR-1999;
23-APR-1999;
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01-APR-1999;
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05-MAY-1999;
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27-MAY-1999;
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                                                                                                                                                                                                                                                                                    Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the gene tuf into tuff encoding a protein resistant to an elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that
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0
                             Vijgenboom E, Heinstra PW;
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                                                                                                                                                                     New protein conferring resistance to elfamycin - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elfamycin resistant actinomycetes; antibiotic resistant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein conferring resistance to elfamycin -
transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 102; DB 13;
Pred. No. 2.9e-08;
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                                                                                                                                                                                                                                          Claim 6; Pages 13-15; 35pp; English.
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                             Bosch L,
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81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
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                             Luiten RGM, Kerkman R,
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                                                                                                WPI; 1992-017874/03
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elongation factor.
                                                                                                                      N-PSDB; AAQ20220
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10-JUL-1990;
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| 90S - 0136782 90S - 0137228 90S - 0137528 90S - 0137502 90S - 0138740 90S - 0138847 90S - 0139845 90S - 0139452 90S - 0139455 90S - 0139455 90S - 0139455 | 9 US- 0139459 9 US- 0139459 9 US- 0139461 9 US- 0139461 9 US- 0139462 9 US- 0139462 9 US- 0139462 9 US- 01398173 9 US- 0140353 9 US- 0140821 9 US- 0140821 9 US- 014287 9 US- 014387 9 US- 014387 9 US- 014387 9 US- 014387 9 US- 014387 9 US- 014387 9 US- 014387 | 990S-0144325. 990S-0144331. 990S-0144334. 990S-0144334. 990S-0144335. 990S-0144352. 990S-014632. 990S-0145086. 990S-0145086. 990S-0145086. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145087. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. |
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes themselves and the encoded proteins. The prokaryotes used are preumoniae, pseudomonas aeruginosa and Enterococcus faecalis. The preumoniae, pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used invention is also useful for the indining to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen corrections can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen correction of a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int, pub/published_pct_sequences.
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                                Gaps
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Length 465;
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                                                                                                                                                                                                                                                                            Enterococcus faecalis cellular proliferation protein #27.
                                Indels
                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
Score 102; DB 21;
Pred. No. 3.5e-08;
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                 Pred. No. 3.5e
0; Mismatches
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                                                                                                                                                                              AAU33391 standard; Protein; 395 AA.
82.9%;
94.7%;
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26-WAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-WOY-2000; 2000US-255625P.
22-DEC-2000; 2000US-257931P.
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                                                               4 KFNRTKPHVNIGTIGHVDH 22
                                                                                  21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                                              (first entry)
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                                18; Conservative
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N-PSDB; AAS51250.
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                 Best Local Similarity
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                                                                                                                                                                                                               AAU33391;
 Query Match
                                Matches
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395 AA;

Sequence

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the inverning relaters to antisense innibitors or genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential conservation is also used in the more and the encoded proteins. The prokaryotes used are send in the encoded proteins. The prokaryotes used are can be send and the encoded proteins to pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The cantibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acid sequence is also useful to screen a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form wipo.int/pub/published_pct_sequences.
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                                       Gaps
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      Length 395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                       Enterococcus faecalis cellular proliferation protein #176.
                                       Indels
                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
11arity 85.7%; Pred. No. 4.3e-08; Conservative 2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Seq ID No 10482; 511pp; English.
                                                                                                                                                                                      AAU34889 standard; Protein; 395 AA.
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2000US-207727P.
2000US-242578P.
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2000US-257931P.
2001US-269308P.
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                                                                                         3 kekfdrskshvnigtighvdh
                                                                      2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis.
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N-PSDB; AAS52748.
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                      Best Local Similarity
Matches 18; Conserv
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26-MAY-2000;
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22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       famamoto RT,
                                                                                                                                                                                                                                                        14-FEB-2002
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          Query Match
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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              132 AA;
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                                                                                                                                                                                                                                          AAY34672;
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                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a cares. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. The acness is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory resence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and activity of P. acnes polypeptides and activity of P. acnes polypeptides and chermining P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes prosence, for example, by carsyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectent.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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                                         Length 395;
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                                       82.1%; Score 101; DB 22; Length 3
85.7%; Pred. No. 4.3e-08;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #27410.
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, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 27709; 1069pp; English.
                                                                                                                                                                                                AAU66514 standard; Protein; 132 AA.
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                                                                                                              3 kekfdrskshynigtighydh 23
                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                      27-FEB-2002 (first entry)
                                                                   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes.
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                                                        Best Local Similarity
395 AA
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                                                                                                                                                                                                                                                                                                                                                                                                              WO200181581-A2.
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07-JUL-2000;
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 Sequence
                                       Query Match
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                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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81.0%; Pred. No. 6.2e-08;
.ive 1; Mismatches 3; Indels (
     Length 132;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia pneumoniae transmembrane protein sequence.
Score 100; DB 22;
Pred. No. 1.8e-08;
; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 675; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                     AAY34672 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; neutralising epitope.
                                                                                                           22
                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
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81.0%;
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97FR-0014673.
                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                           Conservative
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AAU38889;

AAU38889 ID AAU3 XX

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The invention relates to isolated polynucleotide encoding at least a partial Chlamydia protein which is an antigenic fragment, or the complements, fragments, homologues and variants, and antibodies raised against the antigenic proteins (or fragments). The nucleic acids, proteins and antibodies are used to diagnose and treat Chlamydia Infections (e.g. a sexually transmitted disease, pelvic inflammatory disease (PID), acute respiratory tract infection, trachoma, atherosclerosis and coronary heart disease) in a patient, and in the treatment of male infertility. The compounds of the invention are also useful for detecting the presence of Chlamydia in a patient, and stimulating and/or expanding T cells specific for a Chlamydia protein. The present sequence represents a Chlamydia antigen.
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Chlamydia; sexually transmitted disease; PID; antibacterial; pelvic inflammatory disease; antigen; trachoma; gynecological; acute respiratory tract infection; atherosclerosis; male infertility;
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Pred. No. 6.2e-08;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                     Stromberg EJ;
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                                                                                                           Chlamydia trachomatis serovar D.
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81.0%;
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20-JUL-2000; 2000US-219752P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                   coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-616771/71.
                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide encoding at least a partial Chlamydia protein which is an antigenic fragment, or the complements, fragments, homologues and variants, and antibodies raised against the antigenic proteins (or fragments). The nucleic acids, proteins and antibodies are used to diagnose and treat Chlamydia infections (e.g. a sexually transmitted disease, pelvic inflammatory disease (PID), acute respiratory tract infection, trachoma, atherosclerosis and coronary heart disease) in a patient, and in the treatment of male infertility. The compounds of the invention are also useful for detecting the presence of Chlamydia in a patient, and stimulating and/or expanding T cells specific for a Chlamydia protein. The present sequence represents a Chlamydia antigen.
                                                                                                                                                                                       Chlamydia; sexually transmitted disease; PID; antibacterial; pelvic inflammatory disease; antigen; trachoma; gynecological; acute respiratory tract infection; atherosclerosis; male infertility;
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Pred. No. 6.2e-08;
L; Mismatches 3; Indels (
                                                                                                                                                 C. pneumoniae CT322 homologue CPn0074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 147; 208pp; English.
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                 AAU38889 standard; Protein; 394
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Best Local Similarity 81.0%;
Matches 17; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2001; 2001WO-US13081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-2000; 2000US-219752P
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                                                                                                                                                                                                                                                          coronary heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhatia A, Probst P,
                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-616771/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS57020
                                                                                                                                                                                                                                                                                                                                        WO200181379-A2.
                                                                                                         16-JAN-2002
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NAMES OF THE PROPERTY OF THE P

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Sequence

AAU38909,

XEXEXEX

RESULT 28

δ g AAU38909

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by E acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequlate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by once: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. epidermidis open reading frame protein sequence SEQ ID NO:1312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 22;
Pred. No. 6.9e-08;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                     Claim 6; SEQ ID No 1187; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG82109 standard; Protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 kakfertkphonigtighidh 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.3%;
81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-316495/33.
N-PSDB; AAH52959.
                        WPI; 2001-616774/71.
                                          N-PSDB; AAS59510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200134809-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG82109;
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                                                                                                                                                                                                                                                                                                                                                                                   AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, saplingitis, and perihepatitis, bartholinitis; pummopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 20; Length 397;
Pred. No. 6.2e-08;
1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW, Persing DH, Mitcham JL, Wang St
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 735-736; 1755pp; English.
                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU39992 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH 22
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97FR-0015041.
97FR-0016034.
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81.0%;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                            98WO-IB01939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US12865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 81.3
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes.
                                                                                                                                                                                                                                                            WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 AA;
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                                                                                                                                                                       (GEST ) GENSET
                                                                                  04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2000;
07-JUL-2000;
                                          27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
10-JUN-1999
                                                                                                                                                                                                                Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU39992;
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394 AA;
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26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto RT,
                                                                                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
                                                                                       Sequence
                                                                                                                                                                                                                                               AAU34078
                                                                                                                                                                                                                                                                                    8888888888
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                                                                                                                                                                                                q
                                                                   Annology to Annology to represent nucleic actus (1) encouning polypeptides (1) and (11), given in Ad881454 to AA681120, from Staphylococcus epidermidis.

(1) and (11) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (1) may be used to produce the solution of vectors.

S. epidermidis polypeptides (11) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (11) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their reatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AH65090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AH65090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel elongation factors of Staphylococcus aureus useful as antibiotics for treating microbial diseases and infections, comprise a specific
                                                             represent nucleic acids (I) encoding polypeptides
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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                                                                                                                                                                                                                                                                                                                                                            Score 97; DB 22; Length 310;
Pred. No. 1.4e-07;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF-Tu; elongation factor; antibiotic; anti-microbial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus elongation factor Tu.
                                     Page 374; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96769 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 36-37; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                            3 kekfdrskehanigtighvdh 23
                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                            78.9%;
81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                             to AAH53970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequence
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                          310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA51329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2000
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                                     18;
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96769;
                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 32
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                                                                                               for
This is the Staphylococcus aureus elongation factor Tu (EF-Tu). EF-Tu is useful for treating an individual in need of enhanced activity or expression of EF-Tu. EF-Tu is useful as an antibiotic for treating microbial infections and diseases. An antagonist to EF-Tu is useful for treating an individual in need of inhibiting the activity or expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr GJ;
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                                                                                                                                                                                                                                                                                                                  Length 394;
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                                                                                                                                                                                                                                                                                        Score 97; DB 21; Lengtn Jo-
Pred. No. 1.9e-07;
. --*-hes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation protein #354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Seq ID No 5574; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL, Zyskind JW,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU34078 standard; Protein; 394 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
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2000US-206848P.
2000US-207727P.
2000US-242578P.
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2000US-257931P.
2001US-269308P.
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ilarity 81.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
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394 AA;
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06-APR-1999;
08-APR-1999;
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04-MAY-1999;
05-MAY-1999;
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19-MAY-1999;
20-MAY-1999;
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05-MAR-1999;
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06-MAY-1999;
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14-MAY-1999;
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                                                                                                                                      Query Match
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a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protes.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
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                                                                                                                                                Gaps
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Xu HH;
                                                                                                                          Length 394;
                                                                                                                                                                                                                                                                                                             Staphylococcus aureus cellular proliferation protein #1019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                             Score 97; DB 22; Len
Pred. No. 1.9e-07;
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                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                             AAU36849 standard; Protein; 394 AA
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                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                 2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                                          78.9%;
81.0%;
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2000US-207727P.
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                                                                                                                       Query Match 78.99
Best Local Similarity 81.09
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus
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N-PSDB; AAS54708.
                                                                                          394 AA;
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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26-MAY-2000;
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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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Pred. No. 1.9e-07;
2; Mismatches 2; Indels
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99US-0134219
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les 17; Conservative
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| 19999; 19999; 19999; 19999; 19999; 19999; | 10000000000000000000000000000000000000 | | 19999; 19999; 19999; 19999; 19999; 19999; 19999; 19999; |
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02-AUG-1999;
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                                                                                       Gaps
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                                                            Score 96; DB 21; Length 77;
Pred. No. 4.5e-08;
1; Mismatches 1; Indels
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                                                                                                                                                                                               AAG12252 standard; Protein; 86 AA.
 99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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990S-0123180.
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990S-01267864.
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990S-013632.
                                                           Query Match 78.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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29-MAR-1999;
01-APR-1999;
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19-APR-1999;
21-APR-1999;
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28-APR-1999;
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30-APR-1999;
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RESULT 38
AAG12474
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27. AUG-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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Pred. No. 9.8e-08;
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Matches 16; Conservative
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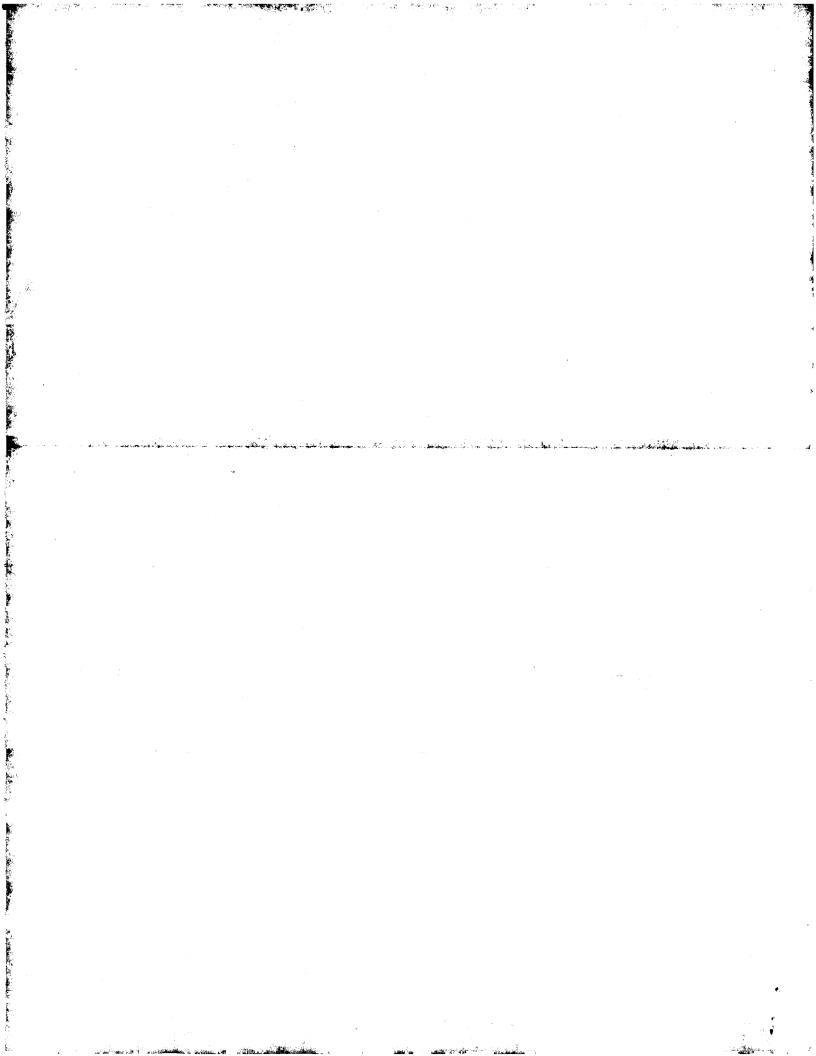
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Gaps

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Search completed: August 22, 2002, 07:44:04 Job time: 63 sec



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P02991
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 100 summaries
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EFTU_BACTR
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EFT2_STRRA
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1 MKEKFNRTKPHVNIGTIGHVDH
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Gapop 10.0 , Gapext 0.5
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EFTU_HELPY

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DECELULAR LOCATION: Cytoplasmic.

-1- SUBGUNT: MONOMER (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

RE-TU/EF-1A SUBFAMILY.

R PIR; B60663; B60663.

R InterPro: IPR000795; GTP_EFTU.D2.

R InterPro: IPR0004161; GTP_EFTU.D2.

R Pfam; PF001049; GTP_EFTU.D2: 1.

R Pfam; PF001049; GTP_EFTU.D2: 1.

R Pfam; PF003144; GTP_EFTU.D2: 1.

R Pfam; PF003145; ELONGATNECT.

R PRINTS; PR00315; ELONGATNECT.

R PRINTS; PR00315; ELONGATNECT.

R PROSITE; PS00301; EFACTOR_GTP; 1.

R PROSITE; PS00301; EFACTOR_GTP; 1.

R PRINTS; PR00315; GTP_EFTU.D3: 1.

R PRINTS; PR00315; ELONGATNECT.

R PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                       Ludwig W., Weizenegger M., Betzl D., Leidel E., Lenz T., Ludvigsen A., Moellenhoff D., Wenzig P., Schleifer K.H.; "Complete nucleotide sequences of seven eubacterial genes coding for the elongation factor Tu: functional, structural and phylogenetic evaluations.";
                                                                                                                                                     Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae; Bacteroides.
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MEDLINE-81165558; PubMed=7011904;
An G., Friesen J.D.;
"The nucleotide sequence of tufB and four nearby tRNA structural genes of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                  THE GTP-DEPENDENT BINDING OF
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Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                        ACCD. MICCODIOL. 153:241-247(1990).
-1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 112; DB 1; Length 39 Pred. No. 5.9e-11; 0; Mismatches 1; Indels
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
7B4C6FD208323149 CRC64;
                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TUF.
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01-MAR-1989 (Rel. 10, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-OGT-2001 (Rel. 40, Last annotation update)
(TUFA OR B3339) AND (TUFB OR B3980).
  394 AA
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    PRT;
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MEDLINE=90240875; Pubmed=2110445;
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394 AA; 43580 MW;
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Best Local Similarity 95.2
Matches 20; Conservative
    STANDARD;
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EFTU_BACFR
P33165;
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P02990;
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MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGraful L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBGNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLIGAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                            Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS PROFEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROFEIN
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
MW; 502751637BDA2707 CRC64;
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Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
PRINTS: PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
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Pred. No. 6.1e-12;
                                  (Rel. 35, Created)
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  399 AA
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  PRT;
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
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100.0%; Pre
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                                                                     16-0CT-2001 (Rel. 40, Last an Elongation factor Tu (EF-Tu)
TUF OR TUFA OR HP1205.
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Nature 388:539-547(1997).
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STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                       NCBI_TaxID=210;
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01-NOV-1997 (
16-OCT-2001 (
                                                                                                                                                                                   Helicobacter
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Best Loral Simi
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Length 394;

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Laursen R.A., L'Italien J.J., Nagarkatti S., Miller D.L.;
"The amino acid sequence of elongation factor Tu of Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      properties of proteins encoded
                                                                                                                                                                                                                             MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-82124558; Pubmed-7035613;
Miyajima A., Shibuya M., Kuchino Y., Kaziro Y.;
Miranscription of the E. coli tufB gene: cotranscription with four
tRNA genes and inhibition by
guanosine-5'-diphosphate-3'-diphosphate.";
                                                                     Daniels D.L.;
"Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
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                                                                                                                         SEQUENCE FROM N.A. (TUFA).
MEDLINE-81165557; PubMed-7011903;
YOKOTA T., Sugisaki H., Takanami M., Kaziro Y.;
"The nucleotide sequence of the cloned tufA gene of Escherichia
                                                                                                                                                                                                                                                                                                                                             Jones M.D., Petersen T.E., Nielsen K.M., Magnusson S., Sottrup-Jensen L., Gausing K., Clark B.F.C.; "The complete amino-acid sequence of elongation factor {\tt Tu} from
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J. Biol. Chem. 268:601-607(1993).
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deprivation in Escherichia coli.";
J. Bacteriol. 173:3096-3100(1991).
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                    SEGUENCE FROM N.A. (TUFB).
STRALN-KL2 / MG1655,
MEDLINE-9400932; Pubmed-8265357;
Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
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"Comparing the predicted and observed p:
in the genome of Escherichia coli K-12.
Electrophoresis 18:1259-1313(1997).
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J. Biol. Chem. 256:8102-8109(1981).
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STRAIN-K12 / EMG2;
                                                                                                                                                                                                         SEQUENCE FROM N.A. (TUFA).
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Sene 12:33-39(1980)
                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                    Daniels D.L.
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"The structural and functional basis for the kirromycin resistance of mutant EF-Tu species in Escherichia coll.";
EMBO J. 13:4877-4885(1994).
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Zhang Y., Yu N.J., Spremulli L.L.;
"Mutational analysis of the roles of residues in Escherichia coll
elongation factor Ts in the interaction with elongation factor Tu.";
J. Biol. Chem. 273:4556-4562(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97133305; PubMed-8978702; Vorstenbosch E., Pape T., Rodnina M.V., Kraal B., Wintermeyer W.; The G222D mutation in elongation factor Tu inhibits the codon-induced conformational changes leading to GFPase activation on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS RESISTANT TO KIRROMYCIN.
MEDLINE-95045380; Pubmed=7525272;
Mesters J.R., Zeef L.A.H., Hilgenfeld R., de Graaf J.M., Kraal B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hwang Y.-W., McCabe P.G., Innis M.A., Miller D.L.; "Site-directed mutagenesis of the GDP binding domain of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-88007508; PubMed=3308869;
Hwang Y.-W., Miller D.L.;
Hwang Y.-W., Miller D.L.;
Fa mutation that alters the nucleotide specificity of elongation
factor Tu, a GTP regulatory protein.";
J. Biol. Chem. 262:13081-13085(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89255270; PubMed-2498311; Hwang Y.-W., Sanchez A., Miller D.L.; Mutagenesis of bacterial elongation factor Tu at lysine 136. A "Mutagenesis of bacterial elongation factor Tu at lysine 136. A conserved amino acid in GTP regulatory proteins."; J. Biol. Chem. 264:8304-8309(1989).
                                                                        L'Italien J.J., Laursen R.A.; "Location of the site of methylation in elongation factor {\tt Tu."}\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeef L.A.H., Bosch L., Anborgh P.H., Cetin R., Parmeggiani A., Hilgenfeld R.; "Pulvomycin-resistant mutants of E.coli elongation factor Tu."; EMBO J. 13:5113-5120(1994).
                                                                                                                                                                                                                                                                                                         Jacquet E., Parmeggiani A.; "Substitution of Val20 by Gly in elongation factor Tu. "Substitution with elongation factors Ts, aminoacyl-tRNA interaction with elongation factors Ts, aminoacyl-tRNA ribosomes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 75-89, AND MUTAGENESIS OF PRO-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS OF HIS-19; GLN-114 AND GLU-348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Biochem. Biophys. 274:394-403(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biochem. 185:341-346(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90025117; PubMed=2508560;
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                                                                                                                                                                                                                                                                 MEDLINE=90060119; PubMed=2684669;
                                MEDLINE=80069392; PubMed=389663;
                                                                                                                                                FEBS Lett. 107:359-362(1979)
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EMBO J. 15:6766-6774(1996).
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MUTAGENESIS OF LYS-136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elongation factor Tu."
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METHYLATION
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HI0578:
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NP_BIND
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EFTU_SALTY
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                        Kjeldgaard M., Nyborg J.; "Refined structure of elongation factor EF-Tu from Escherichia coli.";
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                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: CYTOPLASMIC, AND MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
MEDLINE-99141376; PubMed=9918724;
Song H., Parsons M.R., Rowsell S., Leonard G., Phillips S.E.V.;
Crystal structure of intact elongation factor EF-Tu from Escherichia coli in GDP conformation at 2.05-A resolution.";
J. Mol. Biol. 285:1245-1256(1999).
- PUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMMONORYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                 Leberman R.;
                                                                                                                                                                      Kawashima T., Berthet-Colominas C., Wulff M., Cusack S., Leberman R.;
Nature 381:172-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIZINE—95550630; Pubmed=7542800; Playton R.A., Kirkness E.F., Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.T., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Haemophilus.
                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH EF-TS.
MEDILINE-56170031; Pubmed-8596629;
Kawashima T., Berthet-Colominas C., Wulff M., Cusack S., Lek
"The structure of the Escherichia coli EF-Tu.EF-Ts complex a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 111; DB 1; Length 393;
Pred. No. 8.6e-11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: MAY PLAY AN IMPORTANT REGULATORY ROLE IN IN THE BACTERIAL RESPONSE TO NUTRIENT DEPRIVATION.
                                                                                                                                                                                                                    MEDLINE-97094972; PubMed-8939740;
Abel K., Yoder M.D., Hilgenfeld R., Jurnak F.;
An alpha to beta conformational switch in EF-Tu.";
Structure 4:1153-1159(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
(TUFA OR H10578) AND (TUFB OR H10632).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 AA
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X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=92177415; PubMed=1542116;
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                                              J. Mol. Biol. 223:721-742(1992).
[22]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 90.5
19; Conservative
                                                                                                                                   Nature 379:511-518(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS
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                                                                                                                        resolution.
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P43926;
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Best Local S
Matches 19
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                                                                                                                               BIOSYNTHESIS.

-!-SUBUNIT: MONOMER (BY SIMILARITY).
-!-SUBCELLUIAR LOCATION: CYLOPIASMIC.
-!-SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ASSOCIATED WITH AMINOACYL-TRNA BINDING
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MEDLINE-91002658; PubMed-2207156;
Tuohy T.M.F., Thompson S., Gesteland R.F., Hughes D., Atkins J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
ASSOCIATED WITH GUANOSINE NUCLEOTIDE
                                                                                FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae; Salmonella.
NCBL_raxID=602, 601;
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-2002 (Rel. 41, Last annotation update)
Elongation factor Tu (EF-Tu).
(TUFA OR STM3445 OR STY4353) AND (TUFB OR STM4146 OR STY3739).
Salmonella typhimurium, and
"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.2%; Score 111; DB 1; Length 393; 90.5%; Pred. No. 8.6e-11; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
Pfam; PF03145; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGAUNECT.
PROSITE; PS00301; EFACTOR_GTP;
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                                                       Science 269:496-512(1995).
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P02990; 1ETU.
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Best Local Similarity 90.5
Matches 19; Conservative
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138
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INIT_MET 0
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ASSOCIATED WITH AMINOACYL-TRNA BINDING

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BINDING
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StyGene; SG10403; tufA.
StyGene; SG10404; tufB.
StyGene; SG10404; tufB.
InterPro; IPR00416; GTP_EFTU_D2.
InterPro; IPR00416; GTP_EFTU_D3.
Pfam; PF00309; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNET; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
ELONGATION factor; Protein blosynthesis; GTP-binding; Phosphorylation;
                                                                                                                                                                                                                                         SPECIES-S. Typhi; STRAIN=CT18; MEDLINE-21534947; PubMed=11677608; MEDLINE-21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L. Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brocks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Mowd L., White N., Farrar J., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Typhi CT18.";
                                                                   SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609; MCCLelland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                    "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBUNIT: MONOMER (BY SIMILARITY).
-i- SUBCELLIALIDAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
"The role of EF-Tu and other translation components in determining translocation step size.";
                                                                                                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: THIS PROFEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
METHYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                          Biochim. Biophys. Acta 1050:274-278(1990)
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                                                                                                                                                                                                Nature 413:852-856(2001).
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                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS.
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NP_BIND
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460.3465(2001).
-!- FUNCTION: THIS PROPEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
             ASSOCIATED WITH GUANOSINE NUCLEOTIDE BINDING ACTIVITIES (BY SIMILARITY).
2833061693363BC4 CRC64;
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                                                                                                                                               Score 111; DB 1; Length 393;
Pred. No. 8.6e-11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FP (BY SIMILARITY).

FP (BY SIMILARITY).

OC704405CF5E9A4C CRC64;
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Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-A (EF-Tu-A).
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006173; AAK03441.1; -.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR000161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU,D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PR.NTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                             Ψ¥.
                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                  2 KEKFERTKPHVNVGTIGHVDH 22
                                                                                                                                                     90.2%;
                                                                                                                                                                             90.5%;
                                                                             43152
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Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                     Query Match 90.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                       137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella multocida
                                                                       393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                       137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUFA OR PM1357
                                                                                                                                                                                                                                                                                                                                                                                                                                  EFTA_PASMU
P57939;
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SEQUENCE
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                          BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.; "The chloroplast genome of a chlorophyll a+c-containing alga,
                                                                                                                                                Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBI_TaxID=2839;
                                                                                                                                                                                                                                                                                                                                                                                 Plant Mol. Biol. Rep. 13:336-342(1995).
-I- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-MINOACXL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.6%; Score 109; DB 1; Length 409; 90.5%; Pred. No. 1.9e-10;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 3DDBBBAC190C2009 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
NCBL_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00009; GTP_EFTU; 1. Pfam; PF00104; GTP_EFTU; 1. Pfam; PF03144; GTP_EFTU D2; 1. PRINTS; PR003143; GTP_EFTU D3; 1. PRINTS; PR00315; ELONGATNFCT. PROSTITE; PS00301; EFACTOR_GTP; 1. ELONGATINF GTP; 1. GTP-binding.
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Blongation factor Tu (BF-Tu).
         15-DEC-1998 (Rel. 37, Last annotation update) Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mendel; 13232; ODOS1;TufA;1...
InterPro; IPRO004755; GTP_EFTU_D2.
InterPro; IPRO04161; GTP_EFTU_D2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z67753; CAA91621.1; -.
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                                                                                                Odontella sinensis.
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                                                                                                                                 Chloroplast.
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EFTU_NEPOL
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GIP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-1- FUNCTION: THIS PROTEIN PROMOTES THE GIP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
CS85C9DFA6935559 CRC64;
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Pfam; PF03144; GTP_EFU; I.
Pfam; PF03143; GTP_EFU_D2; I.
PRINTS; PR00315; ELONGATNET.
PROSITE; PS00301; EFACTOR_GTP; I.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
TUFB OR PM1746.
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(Rel. 33, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21145866; PubMed=11248100;
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InterPro; IPR0004795; GTP_EFTU_D.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
43375 MW;
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Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella multocida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-PM70;
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01-FEB-1996
                                                                                                                                                                                                         EFTB_PASMU
P57966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFTU_ODOSI
P49462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
NP_BIND
SEQUENCE
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porcella S.F., Belland R.J., Judd R.C.;
"Identification of an EF-Tu protein that is periplasm-associated and processed in Neisseria gonorrhoeae.";
Microbiology 142:2481-2489(1996).
-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
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SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                        FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HISEP, POSSOGO, IEEU.

InterPro; IPRO00795; GTP_ETTU.

InterPro; IPRO04161; GTP_ETTU.

Pfam; PF00009; GTP_EFTU_D3.

Pfam; PF03144; GTP_EFTU_D2; 1.

Pfam; PF03144; GTP_EFTU_D2; 1.

Pfam; PF03143; GTP_EFTU_D3; 1.

PRINTS; PR00315; ELONGATNET.

PROSTTE; PR00310; EFACTOR_GTP; 1.

Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%; Score 108; DB 1;
90.5%; Pred. No. 2.7e-10;
tive 1; Mismatches 1.
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01-FEB-1996 (Rel. 33, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 AA.
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                                                                                                            SUBUNIT: MONOMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAB75108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 AA; 43593 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y17167; CAA76676.1; -. EMBL; AL139075; CAB75108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEKFNRTKPHVNIGTIGHVDH
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Nature 403:665-668(2000)
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85
139
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Best Local Similarity
Matches 19; Conserv
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                                                                                      BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOSYNTHESIS
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81
136
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P48864;
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NP_BIND
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SO DE RECOCCO COCCO COCO COCCO COCCO
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                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. The Three are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                 Turmel M., Otis C., Lemleux C.; "The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDILINE-20150912; Pubmed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.W., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandram M.A., Rutherford K.M., van Vliet A.H.M.,
Whitchead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Chloroplast, SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. EF-TU/EF-1A SUBFAMILY.
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                                                                                                                                                                                                         Q.
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                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 410;
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
A7A9B0A6E99C1B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000795; GTP_EFTU.
Pfam: PF00009; GTP_EFTU: 1
PRINTS; PR00315; ELONGATNFCT.
PROSTIE; PS00301; EFACTOR GTP: 1.
Elongation factor; Protein biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.6%; Score 109; DB 1;
ilarity 90.5%; Pred. No. 1.9e-10;
Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 AA
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                        MEDLINE=99398694; PubMed=10468594;
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Best Local Similarity
Matches 19; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                 BIOSYNTHESIS
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069303;
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NP_BIND
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SEQUENCE
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InterPro; IPR000795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
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Lang B.F., Burger G., O'Kelly C.J., Cedergren R., Golding G.B.,
Lemleux C., Sankoff D., Turmel M., Gray M.W.;
"An ancestral mitochondrial DNA resembling a eubacterial genome
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
F96799BE63520444 CRC64;
                                                                                                                                                                                                                                                                                                Elongation factor; Protein biosynthesis; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 107; DB 1; Le
85.7%; Pred. No. 3.9e-10;
"Hiematches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor Tu, mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; core jakobids; Reclinomonas.
NCBL_TaxID=48483;
                                                                                                                                                          InterPro; IPRO00795; GTP_EFTU.
InterPro; IPRO04161; GTP_EFTU_D2.
InterPro; IPRO04160; GTP_EFTU_D2.
InterPro; IPRO04160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PR03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF007261; AAD11872.1; -. HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                               43084 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                 EMBL; L36380; AAB41517.2; -.
HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    miniature.";
Nature 387:493-497(1997).
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.0
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=ATCC 50394;
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021245;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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NP_BIND
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    A InterPro; it.

R InterPro; It.

R InterPro; IPR004160; ...

R Ffam; PF03044; GTP_EFTU; 1.

DR Pfam; PF03144; GTP_EFTU_D2; 1.

DR PROSITE; PS00301; EFACTOR_GTP; 1.

DR PROSITE; PS00301; EFACTOR_GTP; 1.

KW Elongation factor; Protein biosynthesis; Mitochondrion; GTP-binding.

TWD_BIND 19 26 GTP (BY SIMILARITY).

TND 81 85 GTP (BY SIMILARITY).

139 GTP (BY SIMILARITY).

139 GTP (BY SIMILARITY).

177 MW; 428202ADF3DBC4EF CRC64;
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MEDLINE=94586062; PubMed=8085791;
Ludwig W., Neumalar J., Klugbauer N., Brockmann E., Roller C.,
Klugbauer S., Reetz K., Schachtner I., Ludwigsen A.,
Blachleiner M., Fischer U., Schleifer K.H.;
Phylogenetic relationships of Bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                                                                                                                                                                                                                                                               Gaps
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-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
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Myxococcales; Cystobacterineae; Cystobacteraceae; Stigmatella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bremaud L., Fremaux C., Laalami S., Cenatiempo Y.; "Genetic and molecular analysis of the tRNA-tufB operon of the myxobacterium Stigmatella aurantiaca"; Nucleic Acids Res. 23:1737-1743(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antonie Van Leeuwenhoek 64:285-305(1993).
-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                          Score 107; DB 1;
Pred. No. 3.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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IPR000795; GTP_EFTU.
IPR004161; GTP_EFTU_D2.
IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFTU_STIAU STANDARD; F P424'9; 053775; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1997 (Rel. 35, Last sequin-16-OCT-2001 (Rel. 40, Last annotation)
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                                                                                                                                                                                                                                                                                                                                                                                                          23
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90.5%;
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Best Local Similarity
Matches 19; Conserv
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FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
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MEDLINE=99039499; PubMed=9823893;
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Best Local Similarity 85.7
Matches 18; Conservative
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                                   BIOSYNTHESIS
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P48865;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tiboni O., Cantoni R., Creti R., Cammarano P., Sanangelantoni A.M.; "Phylogenetic depth of Thermotoga maritima inferred from analysis of the flus gene: amino acid sequence of elongation factor G and organization of the Thermotoga str operon."; J. Mol. Evol. 33:142-151(1991).
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                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 1; Length 396;
Pred. No. 4e-10;
); Mismatches 2; Indels
                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
R -> P (IN REF. 2).
NW -> KP (IN REF. 2).
E -> D (IN REF. 2).
F -> R (IN REF. 2).
V -> L (IN REF. 2).
W -> L (IN REF. 2).
W, B091COAGAA7FF721 CRC64;
                                                                                                                                                                          Elongation factor; Protein biosynthesis; GTP-binding.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga.
                           InterPro; IPRO00795; GTP_EFTU.
InterPro; IPRO04161; GTP_EFTU_D2.
InterPro; IPRO04160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU, 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
PROSTIE; PR00315; ELONGAINFO:
PROSTIE; PS00301; EFACTOR_GTP; 1.
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STRAIN-MSB8 / DSM 3109;
MEDLINE-92015266; PubMed-1920450;
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STRAIN-MSB8 / DSM 3109;
MEDLINE-89232666; PubMed-2714630;
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0J-JAN-1990 (Rel. 13, Created)
30-MAX-2000 (Rel. 39, Last sequinf-Crr-2001 (Rel. 40, Last ann
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90.5%;
EMBL; X76870; CAA54197.1; -.
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Best Local Similarity
Matches 19; Conserv
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376
390
396 /
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              HSSP; P02990;
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NP_BIND
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STRAIN-MADRID E;
MEDLINE-97047977; PubMed-8892818;
SYVANEN A., Aniri H., Jamal A., Andersson S.G.E., Kurland C.G.;
"A chimeric disposition of the elongation factor genes in Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYLOPJASMIC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/PE-1A SUBFAMILY.
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AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.0%; Score 107; DB 1; Length 400;
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73F479FE4F69E9A5 CRC64;
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InterPro: IRR004161; GTP_EFTU.D2.
InterPro: IRR004160; GTP_EFTU_D2.
Pfam: PF03144; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNFCT.
Elongation factor; Protein biosynthesis; GTP-binding;
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GTP (BY SIMILARITY).
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30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
TUF OR RP661.
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                            -:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/DE-1A SUBFAMILY.
                                                                                                                                 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krasny L., Mesters J.R., Tieleman L.N., Kraal B., Fucik V., Hilgenfeld R., Jonak J.;
Hilgenfeld R., Jonak J.;
"Structure and expression of elongation factor Tu from Bacillus stearothermophilus."; 313 and 1998.
J. Mol. Biol. 283:371-381(1998).
                     Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
"The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
Nature 407:757-762(2000).
-- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING ON AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIMTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Geobacillus.NCBL_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
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EMBL, AE002151; AAF30935.1; -.
HSSP; PO2990; IET.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
      MEDLINE=20500219; PubMed=11048724;
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MEDLINE=98443240; PubMed=9769211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
136
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                          BIOSYNTHESIS.
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050306;
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EFTU_BACST
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                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                       -:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLIALIAR LOCATION: CYTOPLASMIC.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
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                                                                                                                             -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.2%; Score 106; DB 1; Length 39
90.5%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S -> T (IN REF. 1).
RAT -> ELQ (IN REF. 1).
W; 510FB2997E389BBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; PR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PR03145; ELONGATNFCT.
PR00315; ELONGATNFCT.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TUF OR UU522.
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STRAIN-ATCC 33697 / SEROVAR 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z54170; CAA90881.1; -. EMBL; AJ235272; CAA15101.1; HSSP; P02990; 1ETU.
                                                                                                            Nature 396:133-140(1998).
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136
198
205
394 AA;
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Best Local Similarity
Matches 19; Conserv
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                                                                                      mitochondria."
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P50068;
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CONFLICT

NP_BIND NP_BIND NP_BIND

SEQUENCE

RESULT 16 EFTU_UREPA

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Bruex A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93188701; PubMed-8446028; Honoze N.T., Bergh S., Chanteau S., Doucet-Populaire F., Honoze N.T., Garnier T., Georges C., Launois P., Limpaiboon T., Newton S., Niang K., del Portillo P., Ramesh G.R., Reddi P., Ridel P.R., Sittisombut N., Wu- Hunter S., Cole S.T., "Nucleotide sequence of the first cosmid from the Mycobacterium leprae genome project: structure and function of the Rif-Str
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MEDLINE-94375410; PubMed-8089081;
Dhandayuthapani S., Banu J.M., Kashiwabara Y.;
Cloning and sequence determination of the gene coding for the elongation factor Tu of Mycobacterium leprae.";
J. Biochem. 115:664-669(1994).
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                                                                                                                                                            Consend an emac.

R EMBL: X77034; CA544323.1; -.

R EMBL: X77034; CA544323.1; -.

R HSSP; PO2990; LETU.

BR InterPro: IPR000155; GTP_EFTU.

BR InterPro: IPR000155; GTP_EFTU.

BR Fam; PF03144; GTP_EFTU_D3.

BR Fam; PF03144; GTP_EFTU_D2; 1.

BR PRINTS; PR00315; ERCNUMPKCT.

BR BINTS; PR00315; ERCNUMPKCT.

BR BINTS; PR00315; EFACTOR_GTP; 1.

RW BLONGation factor; Protein biosynthesis; GTP-binding.

WD BIND

R SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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90.5%; Pred. No. 5.8e-10;
ive 0; Mismatches 2;
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01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Best Local Similarity 90.5
Matches 19; Conservative
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EFTU_MYCLE
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                                                                       -1- SUBCELLULAR LOCATION: CYtOplasmic.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SÜBÜNIT: MONOMER (BY SIMILARITY).
-i- SUBCELLÜLAR LÖCATION: CYLOPLASMIC.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/ZE-1A SUBFAMILY.
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Bachleitner M., Fischer U., Schleifer K.H.;
"Phylogenetic relationships of Bacteria based on comparative sequanalysis of elongation factor Tu and ATP-synthase beta-subunit Antonie Van Leeuwenhoek 64:285-305(1993).

I- FUNCTION: THIS PROFEN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROFEIN
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  AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 1; Length 395;
Pred. No. 5.8e-10;
0; Mismatches 2; Indels
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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71B08165E7FB42C5 CRC64;
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NP_BIND 19 26 GTP (BY SIMILARITY).
NP_BIND 81 85 GTP (BY SIMILARITY).
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Last annotation update)
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                                               SUBUNIT: MONOMER (BY SIMILARITY).
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SEQUENCE FROM N.A.
STRAUN-ATCC 13059 / AS019;
MEDLINE-94368062; PubMed-8085791;
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEGM: PF00009; GTP_EFTU; 1.
Pfam: PF03144; GTP_EFTU_D2; 1.
Pfam: PF03143; GTP_EFTU_D3; 1.
PRINTS: PR00315; ELONGATNECT.
PROSITE: PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ000260; CAA03976.1; -. HSSP; P02990; 1ETU.
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Best Local Similarity 90.5%;
Matches 19; Conservative (
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Gaps

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                            Gaps
                                                                                                                                         -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EE-1A SUBFAMILY.
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Pred. No. 5.8e-10;
0; Mismatches 2; Indels
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GVPYILVALNKSDAPDDEELLELV ->
PWTTRNYSSIS_(IN REF. 2).
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G -> A (IN REF. 2)
R -> P (IN REF. 3)
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                      MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                    InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
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Pfam: PF03144; GTP_EFTU.D2; 1.
Pfam: PF03143; GTP_EFTU_D3; 1.
PROSITE: PS00301; EFACTOR_GTP; 1.
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EMBL; Z14314; CAA78674.1; -.
EMBL; D13869; BAA02982.2; -.
EMBL; AL583923; CAC30831.1; -.
PIR; S34954; S34954.
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90.5%;
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Best Local Similarity 90.5
Matches 19; Conservative
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NP_BIND 19
       SEQUENCE FROM N.A.
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396 A
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NP_BIND
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Carlin N.I.A., Loefdahl S., Magnusson M.;
"Monoclonal antibodies specific for elongation factor Tu and complete
nucleotide sequence of the tuf gene in Mycobacterium tuberculosis.";
Infect. Immun. 60:3136-3142(1992).
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SUBUNTT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONG TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITE-9825987; pubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglandier K., Gas S., Barry C.E. III, Tekaia F., Davies R., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Coliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROFEIN PROMOTES THE GTP-DEPENDENT BINDING
-AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
16-OCT-2001 (Rel. 40, Last annotation
Elongation factor Tu (EF-Tu).
TUF OR RV6685 OR MT0713 OR MTCX210.02.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X63539; CAA45102.1; -.
EMBL; X63539; CAA45101.1; ALT_INIT.
EMBL; 284395; CAB0647.1; -.
EMBL; AE006965; AAK44939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92347983; PubMed-1639483;
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Pfam; PF03144; GTP_EFTU_D2; 1.
PRAM: PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNRCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2
InterPro; IPR004160; GTP_EFTU_D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
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TubercuList; Rv0685; -.
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HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      NCBI_TaxID=1773;
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RESULT 22
EFTU_PSEAE
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                                                                                                                                                                                                                                                                                                                  Bacteria; Protechacteria; beta subdivision; Comamonadaceae; Thiomonas.
NCBL_TaxID-36860;
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94368062; PubMed=8085791;
Ludwig W., Neumaier J., Klugbauer N., Brockmann E., Roller C.,
Klugbauer S., Reetz K., Schachtner I., Ludvigsen A.,
Bachleitner M., Fischer U., Schleifer K.H.;
"Phylogenetic relationships of Bacteria based on comparative sequence
analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBBNIT: MONOMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moreira D., Amils R.; "The str operon from the chemolithotrophic bacterium Thiobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cuprinus.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                            Length 396;
                                                                                                                    2; Indels
                     26 GTP (BY SIMILARITY).
87 GTP (BY SIMILARITY).
141 GTP (BY SIMILARITY).
43593 MW: 85F9012F364692FF CRC64;
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                         86.2%; Score 106; DB 1; 90.5%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                          EFTU_THICU STANDARD; PRT; 396 AA. P42481; 050556; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 10-NOV-1995 (Rel. 40, Last annotation update) Elongation factor Tu (EF-Tu).
                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antonie Van Leeuwenhoek 64:285-305(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P02990; 1ETU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
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Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGAINECT.
                                                                                                                                           2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                        3 KAKFQRTKPHVNIGTIGHVDH 23
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                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                             Thiobacillus cuprinus.
                       19
83
138
396 AA;
                                                                                            Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
             Complete proteome.
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                                                         SEQUENCE
                                 NP_BIND
NP_BIND
                       NP_BIND
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EFTU_THICU
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STRAIN=ATCC 15692 / PRO1;
STRAIN=ATCC 15692 / PRO1;
MEDLING-20437337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-O.T., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Competted genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen ";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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SUBCELLULAR LOCATION: CYCOPLASMIC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-IA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-12 FROM N.A.
MEDLINE=88303352; Pubbled=3136442;
Hughes M.A., Jones D.S.;
Hughes M.A., Jones D.S.;
A fragment of the Pseudomonas aeruginosa genome contains five tRNA genes, four of which are linked to an EF-Tu gene.";
Nucleic Acids Res. 16:7193-7193(1988).
-i. FUNCTION: THIS PROTEIN PROMOTES THE GIP-DEPENDENT BINDING OF AMINOMOCYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                               Length 396;
                                                                                                                                                                                                                                                                                                                                                                        86.2%; Score 106; DB 1; Length 39
85.7%; Pred. No. 5.8e-10;
.ive 1; Mismatches 2; Indels
PROSITE, PS00301; EFACTOR_GTP; 1.

Elongation factor; Protein biosynthesis; GTP-binding.
NP_BIND 19 26 GTP (BY SIMILARITY).
NP_BIND 136 139 GTP (BY SIMILARITY).
CONFLICT 109 109 A -> G (IN REF. 2).
CONFLICT 383 383 G -> A (IN REF. 2).
CONFLICT 387 388 GA -> AG (IN REF. 2).
SEQUENCE 396 AA; 43026 MW; 06D557D04ADB44AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
TURB OR PA4277.
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PIR; S01222; S01222.
InterPro; IPR000795; GTP_EFTU.
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                               Elongation factor; PP BIND 19 NP_BIND 81 IN NP_BIND 136 IN CONFLICT 109 IN CONFLICT 387 3 SEQUENCE 396 AA;
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P09591;
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Gaps

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1- SUBUNIT: MONOMER.

1- SUBULIT: MONOMER.

1- SUBCELLULAR LOCATION: Cytoplasmic.

1- SIMILARIT: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

SIMILARIT: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

BET-TU/EF-1A SUBFAMILY.

R HSSP; F60663; F60663.

R HSSP; P60509; IEPU.

R INTER-PRO; IPR000795; GTP_EFTU.

R INTER-PRO; IPR004161; GTP_EFTU_D2.

R INTER-PRO; IPR04161; GTP_EFTU_D2.

R Ffam; PF003143; GTP_EFTU_D3.

R Pfam; PF031443; GTP_EFTU_D3.

R Pfam; PF031443; GTP_EFTU_D3.

R PRINTS; PR00315; ELONGATNECT.

R PRINTS; PR00315; ELONGATNECT.

R PRINTS; PR00315; ELONGATNECT.

R PRINTS; PR00315; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                                                                                                Ludwig W., Weizenegger M., Betzl D., Leidel E., Lenz T., Ludvigsen A., Moellenhoff D., Wenzig P., Schleifer K.H.;
"Complete nucleotide sequences of seven eubacterial genes coding for the elongation factor Tu: functional, structural and phylogenetic evaluations.";
Arch. Microbiol. 153:241-247(1990).

Arch. Microbiol. 153:241-247(1990).

AMINOACYL. TRIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL. TRIA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaee; Streptococcus.
                                     Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.2%; Score 106; DB 1; Length 398;
85.7%; Pred. No. 5.8e-10;
tive 3; Mismatches 0; Indels
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 82399826C6C08E90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elongation factor; Protein biosynthesis; GTP-binding
                     86.2%; Score 106; DB 1; Le
90.5%; Pred. No. 5.8e-10;
Micmatches 2;
                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90240875; PubMed-2110445;
                                                                                               22
                                                                                                               3 KAKFERTKPHVNIGTIGHVDH 23
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                                                                                              2 KEKFNRTKPHVNIGTIGHVDH
                                                                 Conservative
                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                               Streptococcus oralis.
                                    Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1303;
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16-OCT-2001
16-OCT-2001
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P82559;
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NP_BIND
NP_BIND
SEQUENCE
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EFTU_STRPY
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Matches
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-:- SUBCELLUAR LOCATION: CYTOPLASMIC.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces cinnamoneus.
Batteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_FaxID=53446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cappellano C., Monti F., Sosio M., Donadio S., Sarubbi E.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROPEIN PROMOYDES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                     19 26 GTP (BY SIMILARITY).
81 85 GTP (BY SIMILARITY).
136 139 GTP (BY SIMILARITY).
397 AA: 43369 MW; A019D5BF8EBAB942 CRC64;
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF001009; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PROMITS; PR00315; ELONGATNFCT.
PROSTITS; PS00301; EFAUTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                               Score 106; DB 1; I
Pred. No. 5.8e-10;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (ER-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                  397 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                          3 KEKFERNKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                             86.2%;
ilarity 85.7%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X98831; CAA67349.1; -
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                        Complete proteome.
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TUE89;
                                                                                                                                                                                                                                                                                                                                                                                                EFTU_STRCJ
P95724;
                                                                                                                                                   NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
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Gaps

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                                                                                                                                                                        STRAIN-MAFF303099;
MEDLINE-21082930; PubMed=11214968;
MEDLINE-21082930; PubMed=11214968;
Maneko T., Nakamura Y., Sato S., Sato S., Kaneko T., Rimura T.,
Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochituti Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symblotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                           Mesorhizobium loti.";

DNA Res. 7:331-338(2000)

-!- FUNCTION: THIS PROPEEN PROMOTES THE GTP-DEPENDENT BINDING OF

AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
Elongation factor Tu (EF-Tu).
(TUFA OR MLR0263) AND (TUFB OR MLR0288).
Rhizoblum loti (Mesorhizoblum loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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on factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.4%; Score 105; DB 1; Le
90.5%; Pred. No. 8.4e-10;
uiematches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP002994; BAB47886.1; -.
EMBL; AP002994; BAB47904.1; -.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
Pfam; PF001009; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOG_CTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-NOV-1990 (Rel. 16, Last seq
16-OCT-2001 (Rel. 40, Last ann
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ψ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KGKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 AA; 42713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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80
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                                                                                                                NCBI_TaxID=381;
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P18906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elongation
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NP_BIND
SEQUENCE
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EFTU_MYCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                        STRAIN=SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192664; PubMed=11296296;
Ferretti J.J., McShan W.M., Addic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-JRS4 / Serotype M6;
Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
VanBogelen R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOSYNTHESIS.
-- SUBUNIT: MONOMER (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
--- EF-TU/EF-1A SUBFAMILY.
                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins.";
Submitted (MAY-2000) to the SWISS-PROT data bank.
-!-FUNCTION: THIS PROFEIN PROMOTES THE GTP-DEPENDENT BINDING
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE006516; AAK33586.1; -.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU.D.
InterPro; OFR004161; GTP_EFTU_D2.
Pfam; PF03144; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TP (BY SIMILARITY).

FP (BY SIMILARITY).

PP (BY SIMILARITY).

21E0B20A8DD21AFB CRC64;
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85.7%; Pred. No. 5.8e-10;
ive 3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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GTP
GTP
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           factor Tu (EF-Tu)
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                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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NP_BIND 19
                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                             NCBI_TaxID=1314;
        longation fac
JF OR SPY0611
                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
16-OCT-2001
16-OCT-2001
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Best Local Simi
Matches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFTU_RHILO
0981F7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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RESULT 26 EFTU_RHILO

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                                                                                                                                                                                                    -i- SUBUNIT: MONOMER.
-i- SUBCELLIOLIAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                        Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=42684;
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STRAINESM 40733...
MEDLINE-95374503; PubMed-7646499;
Mikulik K., Zhulanova E.;
"Sequencing of the tuff gene and the phosphorylation pattern of EF-Tul during development and differentiation in Streptomyces collinus producing kirromycin.",
Biochem. Biophys. Res. Commun. 213:454 461(1995).
--- FUNCTION: THIS PROTEIN PROMOTES THE GIP-DEPENDENT BINDING OF
                                                                                                                               OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                SUDMITTED (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 85.4%; Score 105; DB 1; Length 397;
1 Similarity 85.7%; Pred. No. 8.5e-10;
18; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 GTP (BY SIMILARITY).
87 GTP (BY SIMILARITY).
14.1 GTP (BY SIMILARITY).
43781 MW; D27DF957DF1DDF75 CRC64;
                                                Saunders D.C., Harris D., Cerdeno A.M., Parkhill J., Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
116-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-1 (EF-Tu-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X77039; CAA54329 1; -
EMBL; AL161691; CAB81853.1; -
PIR; A41385; 541335.
HSSP; P02990; LETU.
INTERPRO; IPRO00795; GTP_EFTU.
INTERPRO; IPRO04160; GTP_EFTU_D2.
InterPRO; IPRO04160; GTP_EFTU_D3.
Pfan; PF03144; GTP_EFTU_D2; 1.
Pfan; PF03144; GTP_EFTU_D2; 1.
Pfan; PF03144; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGAINFCT.
PROSITE; PS00301; EPACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces collinus.
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397 AA;
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family.
                                                                                                                                                                               BIOSYNTHESIS
                              STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFT1_STRCU
Q53871;
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SEQUENCE
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EFT1_STRCU
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                                                                                              Inamine J.M., Loechel S., Hu P.C.;
"Nucleotide sequence of the tuf gene from Mycoplasma gallisepticum.";
Nucleic Acids Res. 17:10126-10126(1989).
--i- FUNCTION: THIS PROFER THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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                                                                                                                                                                                                                                          SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCARION: CYLOPLASMIC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FE-1A SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.

Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.

NCBI_TaxID=1902;
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MEDLINE=95002104; PubMed=7918656;

van Wezel G.P., Woudt L.P., Vervenne R., Verdurmen M.L.,

Vijgenboom E., Bosch L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSEP, P02990, 1EFU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PROSITE; PR00315; ELONGATAPFOR.
ELONGATION factor; Protein biosynthesis; GTP-binding.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
963E8B93216279F1 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-DOGRATION factor Tu-1 (EF-Tu-1).
TUF1 OR SCD40A.08.
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                                                                       MEDLINE=90098800; Pubmed=2602129; Inamine J.M., Loechel S., Hu P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43099 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 AA;
                                                SEQUENCE FROM N.A.
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Best Local Similarity
Matches 17; Conserv
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P40174;
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SEQUENCE
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Gaps

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-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-4282341; PubMed-8012612; Vijgenboom E., Woudt L.P., Heinstra P.W.H., Rietveld K., van Haarlem J., van Wezel G.P., Shochat S., Bosch L.; "Three tuf-like genes in the Kirromycin producer Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 397,
                                                                                                                                                                                           EMBL, X67057; CAA47442.1; -..
PIR; S23908; S23908.
HSSP; P02990; B120.
InterPro; IPR00795; GTP_EFTU.D:
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
Pfam; PF03144; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D3: 1.
Pfam; PR03145; GTP_EFTU_D3: 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; ERACTOR_GTP; 1.
PROSITE; PS00301; ERACTOR_GTP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
5442152843D4E306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.4%; Score 105; DB 1; 85.7%; Pred. No. 8.5e-10;
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01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-2 (EF-Tu-2).
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Best Local Similarity 85.75
Watches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
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SEQUENCE
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                                              SUBGUNIT: MONOMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
PTM: PHOSPHORYLATED ON THREONINE AND SERINE.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
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-!- SUBCELLIALIDAR LOCATION: CYtoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TQ/DE-1A SUBFAMILY.
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Actinomycetales; Streptomycineae; Streptomyces.
NCBL_TaxID=1925;
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-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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MEDIINE-94282341; Pubmed-8012612;
Vijgenboom E., Woudt L.P., Heinstra P.W.H., Rietveld K.,
Van Haarlem J., van Wezel G.P., Shochat S., Bosch L.;
"Three tuf-like genes in the Kirromycin producer Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

D72A4054CA2EB567 CRC64;
     AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.4%; Score 105; DB 1; Length 397; 85.7%; Pred. No. 8.5e-10;
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InterPro; IPRO04161; GTP_EFTU_D2.
InterPro; IPRO04160; GTP_EFTU_D3.
Pfam; PF000099; GTP_EFTU; 1.
Pfam; PF00109; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU,D3; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNFCT.
PROSTTE; PR003101; EFACTOR_GTP; 1.
Elongation factor; Protein blosynthesis; GTP-binding; Multigene family; Phosphorylation.
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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-1 (EF-Tu-1).
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                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S79408; AAC60496.1; -.
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386
397 AA;
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MOD_RES
SEQUENCE
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Matches
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-!- SUBCELLIAURA LOCATION: CYtOPLASMIC.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weiser J., Kormanec J., Potuckova L., Homerova D., Vohradsky J., Novotna J., Kalachova L.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases:
-!- FUNCTION: THIS PROPIEIN PROMOYES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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85.7%; Pred. No. 8.5e-10;
ive 1; Mismatches 2; Indels
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P (BY SIMILARITY).
B77172DD423623AD CRC64;
                                                                                                                                                                                                                                                                                                                  Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
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15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 AA.
                                                  HSSP; P02990; IETU.
InterPro; IPR000195; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
Pfam; PF03144; GTP_EFTU; I.
Pfam; PF03144; GTP_EFTU_D2; I.
Pfam; PF03145; GTP_EFTU_D3; I.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; I.
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
InterPro; IPR004160; GTP_EFTU_D3.
InterPro; IPR00414; GTP_EFTU_D1.
InterPro; IPR03143; GTP_EFTU_D2; IPR03143; GTP_EFTU_D2; IPR0315; ELOWGATNFCT.
INTERPROSTITE; PR00310; EFACTOR_GTP; I.
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STRAIN=ATCC 10762 / CCM 3239;
  EMBL; X67058; CAA47443.1; -.
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                                ; $23909.
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138 1
397 AA;
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Best Local Similarity
Matches 18; Conserv
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                             PIR; S23909
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033594;
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SEQUENCE
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Toledo H., Jerez C.A.;
Toledo H., Jerez C.A.;
"In vivo and in vitro methylation of the elongation factor EF-Tu from Euglenn gracilis chloroplast.";
FEMS Microbiol. Lett. 59:241-246(1990).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Montandon P.-E., Stutz E.; "Notation gracilis chloroplast genome region "Nucleotide sequence of a Euglena gracilis chloroplast genome region coding for the elongation factor Tu; evidence for a spliced mRNA."; Nucleic Acids Res. 11:5877-5892(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Chloroplast.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88040410: PubMed-3118328;
Montandon P.-E., Knuchel-Aegerter C., Stutz E.;
"Euglena gracilis chloroplast DNA: the untranslated leader of tufA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the ribosomal proteins S12 and S7 are clustered with
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                                                                                                                         Score 105; DB 1; Length 397;
Pred. No. 8.5e-10;
1; Mismatches 2; Indels
Protein biosynthesis; GTP-binding.
26 GTP (BY SIMILARITY).
87 GTP (BY SIMILARITY).
1411 GTP (BY SIMILARITY).
43509 MW; A22F12F0E3008EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                           409 AA.
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Nucleic Acids Res. 15:7809-7822(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 12:2851-2859(1984).
                                                                                                                                                                                                                                                                                                                             PRT;
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SEQUENCE OF 1-28 FROM N.A.
MEDLINE=84169577; PubMed=6324129;
Montandon P., Stutz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83299257; PubMed-6310519;
                                                                                                                                                                                                                  3 KAKFERTKPHVNIGTIGHIDH 23
                                                                                                                                                                                                 2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                           85.4%;
                                                                                                                         Query Match 85.4°
Best Local Similarity 85.7°
Matches 18; Conservative
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                  19
83
138 1
397 AA;
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SEQUENCE FROM N.A.
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ID EFTU_EUGGR
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                                                  NP_BIND
SEQUENCE
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                                     NP_BIND
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inamine J.M., Loechel S., Hu P.-C.;
"Nucleotide sequence of the tuf gene from Mycoplasma genitalium.";
Nucleic Acids Res. 17:10127-10127(1989).
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STRAIN-AFCC 35330 / G-37;
MEDLINE-940/5230; Pudde-8253680;
PEterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
I -> M (IN REF. 2).
O9B73EADCAODF5F6 CRC64;
                                                                                                                                                                                                                       InterPro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; 1.
PRINTS; PR00315; ELONGAINFCT.
PROSTITE; PS00301; EFACTOR GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104; DB 1; L. Pred. No. 1.2e-09; 2; Mismatches 2;
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PETU_MYCGE STANDARD; PRT; 394 AA.
213327; 049360;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
TUF OR MG451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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STRAIN=ATCC 33530 / G-37;
MEDLINE-90098801; Pubmed=2602130;
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STRAIN-ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
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81 85 GT
136 139 GT
89 89 I
394 AA; 43465 MW;
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NCBI_TaxID=2097;
                                                                                                                                                                                   EMBL; Y12307; CAA72974.1; -. HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.6%;
81.0%;
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Best Local Similarity 81.0
Matches 17; Conservative
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EFTU_MYCGE
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SUBCELLULAR LOCATION: CYtoplasmic.
SIMILARITY: BELONGS TO THE GIP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FE-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Puchhara an Apg".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98242088; PubMed=9580987;
MEDLINE=98242088; PubMed=9580987;
Brynnel E.U., Kurland C.G., Moran N.A., Andersson S.G.;
Evolutionary rates for tuf genes in endosymbionts of aphids.";
Mol. Biol. Evol. 15:574-582(1998).
-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

METHYLATION (MONO-) (PROBABLE).

C803740422FFEB84 CRC64;
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81.0%; Pred. No. 8.8e-10;
tive 3; Mismatches 1; Indels
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Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                              Elongation factor; Protein biosynthesis; Chloroplast; GTP-binding; Methylation.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
  or send an email to license@isb-sib.ch)
                               EMBL; 211874; CAA77904.1; --
EMBL; X00044; CAA2925.1; --
EMBL; X00810; CAA50999.1; --
EMBL; X00810; CAA50097.1; --
EMBL; X00480; CAA5159.1; --
PIR; A03319; EFEGT.
PIR; S0254; S0254.
PIR; S34508; S34508.
HSSP; P02990; 1ETU.
MAGGI, 4838; EUGGr; TuffA;1.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004160; GTP_EFTU.
InterPro; IPR004160; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D3;
Pfam; PF03144; GTP_EFTU_D3;
PRINTS; PR00314; ELONGAINFCT.
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81 85 GTI
136 139 GTI
136 139 GTI
57 BME
409 AA; 45062 MW; (
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Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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031297;
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SEQUENCE
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Matches
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Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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81
136
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                                                                pneumoniae.'
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P33167;
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1D EFTU_B
1D 973167
DT 01-0CT
DT 16-0CT
DE ELONG
DR TUF.
0C BURKhC
0C BURKhC
0C BURKhC
0C BURKhC
0C ROCC
NO ROCC
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                            SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYtoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EP-TU/FE-1A SUBFAMILY.
FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-91125132; Pubmed=2126326;
Yogev D., Sela S., Bercovier H., Razin S.;
Nucleotide sequence and codon usage of the elongation factor Tu(EF-Tu) gene from Mycoplasma pneumoniae.";
Mol. Microbiol. 4:1303-1310(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.6%; Score 104; DB 1; Length 394; 76.2%; Pred. No. 1.2e-09; ive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
T -> N (IN REF. 3).
N; 3F62C644A40E49DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFTU_MYCPN STANDARD; PRT; 394 AA. P23566; P75126; Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) TUF OR MPN665 OR MP177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGAINECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; Pubmed=8948633;
                                                                                                                                                                                                                                                                                                                   EMBL, X16463; CAA34483.1; -... EMBL; U39732; AAB01641.1; -... EMBL; U39272; AAD12520.1; -... EMBL; U02255; AAD12520.1; -... EMBL; U02299; EFYMTG. HSSP; P02990; IETU. TIGR; MG451; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000795; GTP_EFTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 REKFDRSKPHVNVGTIGHIDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                       BIOSYNTHESIS
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CONFLICT
SEQUENCE
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EFTU_MYCPN
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Matches
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

HV -> QL (IN REF. 1).

S -> I (IN REF. 1).

L -> V (IN REF. 1).

EWIPTPEREVUK -> DGFQLLNVKWTN (IN REF. 1).

E -> V (IN REF. 1).

T -> S (IN REF. 1).

T -> S (IN REF. 1).

E-> V (IN REF. 1).

E-> V (IN REF. 1).

E-> S (IN REF. 1).

EVLE -> KCLNSESRILSWLC (IN REF. 1).

EVLE -> KCLNSESRILSWLC (IN REF. 1).
"Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                           SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                Fucleic Acids Res. 24:4420-4449(1996).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.6%; Score 104; DB 1; Length 394; 76.2%; Pred. No. 1.2e-09; ive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X55768; CAA39292.1; -.
EMBL; AE000019; AAB95825.1; -.
EMBL; AE000019; EMBPS P02990; IETU.
HSSP; P02990; IETU.
InterPro; IPR004161; GTP_EFTU.
InterPro; IPR04160; GTP_EFTU_D2.
InterPro; IPR04160; GTP_EFTU_D2.
Pfam; PF03144; GTP_EFTU_D2; I.
Pfam; PF03144; GTP_EFTU_D2; I.
Pfam; PF03145; GTP_EFTU_D3; I.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EACTOR_GTP; I.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-077-1993 (Rel. 27, Created)
01-077-1993 (Rel. 27, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 REKFDRSKPHVNVGTIGHIDH 23
                                                                                                                                                                                                                                             EF-TU/EF-1A SUBFAMILY.
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85
139
139
122
122
209
209
360
394
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391
394 AA;
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
NP_BIND 19
NP_BIND 81
                                                                                                                                    BIOSYNTHESIS.
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PRT;
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MEDLINE-94368062; Pubmed-8085791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; CFB group; Taxeobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KEKFNRTNPHVNIGTIGHVYH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.6%;
90.5%;
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85
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                                                                                                                                                                                                                                                                                                                                                                                                       136 1
399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFTU_TAXOC P42480;
                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
NP_BIND
SEQUENCE
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EFTU_TAXOC
     q
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                     Leidel E., Lenz T., Ludvigsen A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                           for
                                                                                                                                                                                    -1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
PIR; D60663; D60663.
HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS.
SUBUNT: MONOMER (BY SIMILARITY).
SUBCLIU: MONOMER (BY SIMILARITY).
SUBCELLUIAR LOCATION: Cytoplasmic.
SIMILARITY: BELONG TO THE GTP-BINDING ELONGATION FACTOR FAMILY
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
               Ludwig W., Welzenegger M., Betzl D., Leidel E., Lenz T., Ludvigser Moellenhoff D., Wenzig P., Schleifer K.H.; "Complete nucleotide sequences of seven eubacterial genes coding the elongation factor Tu: functional, structural and phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q.
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                                                                                                                                     BINDING
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                                                                                                             Arch. Microbiol. 153:241-247(1990).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-AMINOACYL TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104; DB 1; Length 39:
Pred. No. 1.2e-09;
Pred. Totches 2; Indels
                                                                                                                                                                                                                                                                                            HASEY, FULZJU, 161.1.
HIGETPO: IPRO00795; GTP_EFTU.D.
InterPro: IPR004161; GTP_EFTU_D2.
InterPro: IPR004160; GTP_EFTU_D2.
Pfam: PF00109; GTP_EFTU_D2; 1.
Pfam: PF00144; GTP_EFTU_D2; 1.
Pfam: PF00143; GTP_EFTU_D2; 1.
PRINTS: PR00315; ELONGATHEPT.
PROSTIE: PS00315; ELONGATHEPT.
PROSTIE: PS00301; EFACTOR_GTP; 1.
PRINTS: PR00301; EFACTOR_GTP; 1.
PRINTS: PR003119; EFACTOR_GTP; 1.
PROSTIE: PS00301; EFACTOR_GTP; 1.

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136 139 GTP (BY SIMILARITY).
396 AA; 42876 MW; EE21378647AFD644 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
TUF OR TUFA OR JHP1128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
MEDLINE=90240875; PubMed=2110445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.68;
85.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                          BIOSYNTHESIS.
                                                                                               evaluations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFTU_HELPJ
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SEQUENCE
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EFTU_HELPJ
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLUAR LOCATION: CYtoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
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-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 399;
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                                                                                                                                                                                                                                                      EMBL; AE001541; AAD06711.1; -.
HSSP; P0290; IETU.
InterPro; IPR00405; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF0009; GTP_EFTU_1.
Pfam; PF03144; GTP_EFTU_D2.
Pfam; PF03144; GTP_EFTU_D2: 1.
Pfam; PF03144; GTP_EFTU_D2: 1.
PROSITE; PR00315; ELONCATHRCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
4E72A877BFCD104B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NoV-1995 (Rel. 32, Created)
10-NoV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ludwig W., Neumaier J., Klugbauer N., Brockmann E., Roller C., Klugbauer S., Reetz K., Schachtner I., Ludwigsen A., Bachleitner M., Fischer U., Schleifer K.H.; "Phylogenetic relationships of Bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLUAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF
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-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.7%; Score 103; DB 1; Length 395;
85.7%; Pred. No. 1.8e-09;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpetosiphon aurantiacus (Herpetosiphon giganteus). Bacteria; Green non-sulfur bacteria; Chloroflexaceae group; Herpetosiphon. NCBL_raxID=65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                  Elongation factor; Protein biosynthesis; GTP-binding. NP_BIND 19 26 GTP (BY STWILARTY). NP_BIND 81 85 GTP (BY STWILARTY). GTP (BY STMILARTY). SEQUENCE 395 AA; 43038 MW; 168222411386D156 CRC64;
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01-NoV-1995 (Rel. 32, Last sequence update)
01-COT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 AA.
                                                    InterPro; IPR00095; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PR03143; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNET.
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MEDLINE=94368062; PubMed=8085791;
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KETFDRSKPHVNIGTIGHVDH 23
EMBL; X77036; CAA54325.1; -. HSSP; P02990; 1EFU.
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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SEQUENCE FROM N.A.
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P42477;
                                                                                                                                                                                                                                                                                                                                 NP_BIND
NP_BIND
NP_BIND
SEQUENCE
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DR Pfam; PF03143; GTP_EFTU_D3; 1.

DR PRINTS; PR00315; ELONGATNECT.

DR PROSITE; PS00301; EFACTOR_GTP; 1.

KW ELONGATION factor; Protein blosynthesis; GTP-binding.

FT NP_BIND 81 85 GTP (BY SIMILARITY).

FT NP_BIND 136 139 GTP (BY SIMILARITY).

FT NP_BIND 136 43738 MW; 02A543425AD66686 CRC64;

SQ SEQUENCE 400 AA; 43738 MW; 02A543425AD66686 CRC64;

Query Match 83.7%; Score 103; DB 1; Length 400;

Best Local Similarity 81.0%; Pred. No. 1.8e-09;

Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KEKFNRTKPHVNICTIGHVDH 22

|:|| | | | | | | | | | | | |

Db 3 KOKFERNKPHINIGTIGHVDH 23

Search Completed: August 22, 2002, 07:45:38

Job time: 157 sec
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| P45737 bacteroides P44390 haemophilus 097492 canis famil 064405 cavia porce | | USPCS Diagramio P04762 rattus norv P12365 zea mays (m Q59170 brucella me | 027710 onchocerca 09x576 rhizobium m 068146 vibrio fisc 09wv87 rattus norv | P07145 ipomoea bat Q9xzd5 toxoplasma P48351 cucurbita p | P48352 cucurbita p Q9pwf7 rana rugosa | P49315 nicotiana p Q9xhh3 lycopersico | 1997388 HOMO SAPTER P36625 schizosacch Q9axh0 avicennia m | 061235 caenorhabdi P00432 bos taurus Q59602 nelsseria g P24270 mus musculu | | はひコ | | Q9m516 capsicum an P55311 solanum mel P31554 escherichia | P07770 acinetobact P55303 aspergillus | Q926x0 listeria in P24168 listeria se P33569 strentomyce | Q10614 mycobacteri P78753 schizosacch | 015296 homo sapien | homod | bacillus s | schizosacc | Q92405 aspergillus P31449 escherichia | 092598 streptomyce | P74872 salmonella | . 046522 b cytochrom p21179 escherichia | | | 2 4 | Q61093 m cytochrom P24597 mouse polyo | P14726 hordeum vul | | | |
|--|------------------------|---|--|---|--|--|---|---|------------------------------|---|------------|--|--|--|--|--------------------|--------------------|-------------------|--|--|--------------------|--------------------|--|-----------|--------------|------|--|--|----------------------------|----------------|----------|
| 1 CATA_BACFR 1 CATA_HAEIN 1 CATA_CANFA 1 CATA_CAVPO | | | | | | 1 CAT1_NICPL 1 CAT2_LYCES 1 NOV1 HIMAN | | | 1 CATA_ASCSU 1 CAT2_RICCO | | | | | 1 CATA_LISIN 1 CATA_LISSE 1 RCA STRVI. | | | 1 WN8D_HUMAN | | 1 GLH1_CAEEL 1 ORC4_SCHPO | | | | 1 C24B_BOVIN | | 1 YOKI_BACSU | | | | ALIGNMENTS | | |
| 486 508 526 526 | 492 | 526 4 4 9 1 6 9 8 | 482 482 563 | 492 502 492 | 492 527 | 485 | 339 492 | 496 506 526 | 541 492 | 513 4 4 9 2 5 2 2 3 | 492 492 | 492 492 784 | 169 730 | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 456 556 | 354 | 355 | 547 | 972 | 728 307 | 487 | 623 | 570 | 433 | 468 | 269 | 570 648 | 455 | | | |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 40.8 8.0.8 | 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 888 88.00 8.00 8.00 | 38.2 38.2 37.6 | 37.6 | 9.00 0.00 0.00 | 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 36.3 35.7 35.7 | 35.7 | 34.4 | 34.4 | 34.4 34.4 34.4 | 33.8 33.4 | 33.1 | 31.2 | 31.2 | 30.6 | 30.6 | 30.6 | 30.3 29.9 | 29.9 | 29.9 | 29.6 | 29.3 | 29.3 | 29.3 | 29.3 | 29.0 | | | |
| 65 65 65 65 | 4 4 5 | 4 4 6 6 6 6 4 4 6 6 6 6 6 6 6 6 6 6 6 6 | 62 61 61 | 9 20 20 20 | 0 0 0 0 | | 57 | 57 57 56 56 | 55 55 | ស្រួល ស ស្រួក ក្រុ | 24 24 | 5 5 4 5 4 4 | 53 52.5 | 52 | 44 | 4 4 0 0 | 84. | 4.4 | 4.4 | 47.5 | 47 | 4 4 | 46.5 | 46 | 46 | 4.6 | 4 P 4 6 | 45.5 | | | ٦ |
| 34 35 37 | 8 6 6 | 4 4 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 4 3 4 4 4 3 4 | 44 45 74 74 | 48 50 50 | 52 | 5.45 | 57 | 58 59 60 61 | 63 | 64 65 66 67 | 89 9 | 70 71 72 | 73 | 75 | 78 | 80 | 82 | 980 | 98 | 88 | 68 0 | 91 | 92 | 94 | 95 | 97 | 86 6 | 100 | | | RESULT |
| n Ltd. | | Search time 13.53 Seconds (without alignments) 82.991 Million cell updates/sec | | | | 105224 | | | | cted by chance to have a of the result being printed, score distribution. | | Description | Q9zkx5 helicobacte | | 9611 | P55308 hordeum vul | P55310 secale cere | P48350 cucubita p | P23819 arabidopsis P55307 hordeum vul | P55313 triticum ae 092n99 desulfovibr | | P26901 bacillus su | н | oryza sat | | 10 | | Q59714 pseudomonas P29756 qlycine max | ם בי | 339 | 040 homo |
| GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen | search, using sw model | 2, 07:45:38 ; | US-09-488-737-2 157 1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29 | BLOSUM62 Gapop 10.0 , Gapext 0.5 | 224 seqs, 38719550 residues | satisfying chosen parameters: | h: 0 h: 2000000000 | Minimum Match 0% Maximum Match 100% Listing first 100 summaries | SwissProt_40:* | or of results predi equal to the score ysis of the total | SUMMARIES | y h Length DB ID | 505 1 CATA | 0 505 1 CATA_HELPY 2 484 1 CATA_PROMI 1 482 1 CATA_RORPE | 491 1 496 1 | 494 1 CAT2 | 492 1 | 492 | 492 1 | 492 | 492 1 | 482 1 | 4 9 4 9 4 9 4 9 4 | 492 1 | 492 | 492 | 492 I 494 I | , , , , | 492 1 CAT3_ 492 1 CAT3_ | 492 1 502 1 | 26 1 |
| jö | protein - protein | August | US-(score: 157 e: 1 MV | table: BLOSUI Gapop | 105224 | er of hits | DB seq length: DB seq length: | Post-processing: Mini Maxi List | Swit | Pred. No. is the numbe score greater than or and is derived by anal | | % Query Score Match | 57 100. | 93 59.2 | .5 53 | 50. | 44 | 47. | 47. | 46. | 4.6 | | 45. | 44 | 43. | 43. | 4.3. | 42. | 42. | 42. | 42. |

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                                                                                                                                                                                                                                                                                                       STRAIN-26695 / ATCC 700392;
MEDLINE-97394467 PubMed-9252185;
Tonb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Gotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-i- CATALYTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.
-i- COFACTOR: HEME GROUP.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                     MEDLINE-98207782; PubMed-9546115;
Manos J., Kolesnikow T., Hazell S.L.;
"An investigation of the molecular basis of the spontaneous
occurrence of a catalase-negative phenotype in Helicobacter pylori.";
Helicobacter 3:28-38(1998).
                                                                                                                                                                                                                           Odenbreit S., Wieland B., Haas R.; "Cloning and genetic characterization of Helicobacter pylori catalase and construction of a catalase-deficient mutant strain."; J. Bacteriol. 178:6960-6967(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGAND (BY SIMILARITY).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S -> F (IN REF. 1
Y -> I (IN REF. 2
Y -> H (IN REF. 2
N -> D (IN REF. 2
F -> Y (IN REF. 2
L -> Y (IN REF. 2
A -> V (IN REF. 1
                                                                                                                                                                                                              MEDLINE-97113460; PubMed-8955320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U67458; AAC16068.1; -.
EMBL; Z70679; CAA94567.1; -.
EMBL; AE000597; AAD07923.1; -
HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
1129
339
339
234
237
248
255
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313
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ACT_SITE 56
ACT_SITE 129
BINDING 339
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                          SEQUENCE FROM N.A.
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1129
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234
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                            NCBI_TaxID=210;
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                    MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.S.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso G., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                       "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
475A07EF6EEF9B309 CRC64;
                                                                                                                    Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM: PD00510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 157; DB 1; 100.0%; Pred. No. 4.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT, 505 AA. P77872; P94823; STANDARD; PRT; 505 AA. P77872; P94823; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O-CT-2001 (Rel. 40, Last annotation update) Catalase (EC 1.11.1.6). KATA OR HP0875.
                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001510; AAD06391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58527 MW;
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ACT_SITE 56
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=85963;
                                                                                                     KATA OR JHP0809
                                                                                                                                                     Helicobacter
              CATA_HELPJ
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BINDING
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                            09ZKX5;
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P42321
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                                                                                                                                                              CATA_BORPE
P48062;
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BINDING
SEQUENCE
                                                                                                                            CATA_BORPE
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   Matches
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                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXYGEN; S
PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buzy A., Bracchi V., Sterjiades R., Chroboczek J., Thibault P., Gagnon J., Jouve H.-M., Hudry-Clergeon G., "Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of a methionine sulfone in the close proximity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRODENT, PONOUGIO, CATALASE, 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
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                                                                        Length
 -> T (IN REF. 2).
9F029B55B73C26EA CRC64;
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                                                                    Score 157; DB 1;
Pred. No. 4.3e-16;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHIONINE SULFONE.
                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-NOV-1997 (Rel. 35, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                    484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND SEQUENCE OF 1-305 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                             53
                                                                                                                                                               1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                             1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95305957; PubMed=7786407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95311317; PubMed=7791219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Protein Chem. 14:59-72(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 2CAE; 08-DEC-96.
PDB; 2CAF; 07-DEC-96.
PDB; 2CAF; 11-JAN-97.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
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54
127
337 PR
55614 MW;
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                                                                    100.0%;
100.0%;
 316 S
58629 MW;
                                                                                                         Conservative
                                                                                                                                                                                                                                                                    STANDARD;
 316 3
505 AA;
                                                                 Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 AA;
                                                                                                                                                                                                                                                                                                                                                                                           Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=584;
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                                                                                                                                                                                                                                                                  CATA_PROMI P42321;
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ACT_SITE
CONFLICT
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                                                                                                                                                                                                                                  RESULT 3
CATA_PROMI
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Length 484;

Score 93; DB 1; Pred. No. 1.9e-06;

59.2%; 82.6%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deshazer D., Wood G.E., Friedman R.L.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
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    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR0019226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE; 1.
PROSITE; PS00437; CATALASE_1: 1.
PROSITE; PS00438; CATALASE_2: 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.1%; Score 88; DB 1; Length 482; Best Local Similarity 65.5%; Pred. No. 1.1e-05; Matches 19; Conservative 3; Mismatches 5; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROXIMAL HEME LIGAND (BY 7CB73E08975C219F CRC64;
    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Catalase isozyme A (EC 1.11.1.6) (CAT-A).
                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491 AA
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BY SIMILARITY.
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
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                                              7 KQTTAFGAPVWDDNNVITAGPRG
                                                                            S KLTTAAGAPVVDNNNVITAGPRG
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130
340
482 AA; 547
    19; Conservative
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                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BP504;
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NCBI_TaxID=4577
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                             Higo K., Higo H.;
"Cloning and characterization of the rice CatA catalase gene, a homologue of the maize Cat3 gene.";
Plant Mol. Biol. 30:505-521(1996).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                        -:- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-:- COFACTOR: HEME GROUP.
-:- SUBBUIT: HOMOTETRAMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: PEROXISOMEL and 91yoxysomel (By similarity).
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                   Mori H., Higo K., Higo H., Minobe Y., Matsui H., Chiba S.;
"Nucleotide and derived amino acid sequence of a catalase cDNA
isolated from rice immature seeds.";
Plant Mol. Biol. 18:973-976(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; ir...

InterPro; ir...

Pfam; PR00199; catalase, ...

R PRINTS; PR00067; CATALASE.

JR PROSITE; PS00437; CATALASE_1; 1.

DR PROSITE; PS00438; CATALASE_2; 1.

KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; ...

Froxisome; Glyoxysome; Multigene family.

65 65 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

DR PROSITE: PS00438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.2%; Score 83.5; DB 1; Length 491; 61.5%; Pred. No. 5.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 -> PL (IN REF. 2).
5BA4CD73A9F4B748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 16, Created)
(Rel. 33, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@lsb-sib.ch).
                                                                            STRAIN-CV. INDICA; TISSUE-Immature seed;
MEDLINE-92256818; PubMed-1581574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 DVKQTTA-FGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                        STRAIN-CV. JAPONICA; TISSUE-Leaf;
MEDLINE-96189265; PubMed~8605302;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X61626; CAA43814.1; -.
EMBL; D29966; BAA06232.1; -.
PIR; S20873; CSRZ.
HSSP; P00432, 4BLC.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56606 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.2
Best Local Similarity 61.5
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 4
491 AA;
Oryza sativa (Rice)
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                          SEQUENCE FROM N.A
                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                  PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAT3_MAIZE
P18123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Blophys. Acta 951:104-116(1988).

I blophys. Acta 951:104-116(1988).

I blophys. Acta 951:104-116(1988).

I brothor. BECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE. ITS LEVELS ARE HIGHEST IN THE LIGHT PERIOD AND ARE LOWEST IN THE DARK PERIOD, HENCE MAY BE IMPORTANT FOR SCAVENGING HYDROGEN PEROXIDE AT NIGHT, THAN DURING THE DAY.

I COFACTOR: HENE GROUP.

I SUBUNIT: HOMOTETRAMER.

I SUBUNIT: HOMOTETRAMER.

I TISSUE SPECIFICITY: LAFF MESOPHYLL CELLS, PERICARP, SEEDLING ROOTS AND THE COLEOPTILE.
                                                                                         Zea mays (Maize).
Eukaryoch; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
-1- COUTTON: THERE ARE TWO EMBL ENTRIES THAT CORRESPOND TO THE REF.2 SEQUENCE AND THEY ENCODE SLIGHTLY DIFFERENT PROTEINS (SEE THE FEATURE TABLE).
                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and characterization of a genomic sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CV. W64A; TISSUE=Epicotyl;
MEDLINE=89051000; PubMed=2461221;
Redinbaugh M.G. Wadsworth G.J., Scandallos J.G.;
"Characterization of catalase transcripts and their differential expression in maize.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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BY ON REF. 2).

C -> S (IN REF. 2).

T -> Q (IN REF. 2).

H -> P (IN REF. 2).

R -> P (IN REF. 2).

R -> P (IN REF. 2).

P -> A (IN REF. 2).

D -> H (IN REF. 2).
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Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PPODOM; PD00051; CATALASE.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Mitochondrion; Multigene family.
01-FEB-1996 (Rel. 33, Last annotation update)
Catalase isozyme 3 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                           STRAIN-CV. W64A; TISSUE-Seedling leaf; MEDLINE-94003062; PubMed-8400123;
                                                                                                                                                                                                                                                                                                                                                                                                                                    maize Cat3 catalase gene.";
Plant Mol. Biol. 22:1031-1038(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L05934; AAC37357.1; -. EMBL; M31103; AAA33441.1; -. EMBL; X12539; CAA31057.1; -. PIR; JA0091; JA0091. HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                        Abler M.L., Scandalios J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
351
57
79
107
110
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1116
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
351
57
79
110
1112
1115
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PROXIMAL HEME LIGAND (BY SIMILARITY). 67E3CF2AD02E542E CRC64;

56913 MW;

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Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                ACT_SITE 65 65 BY SIMILARITY.
ACT_SITE 138 138 BY SIMILARITY.
                                       65
138
348
494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE004841; AACHSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                    KATA OR PA4236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=FRD1
                                                                                                                                                                                                                                                                                                                              CATA_PSEAE
                                                       ACT_SITE
BINDING
                                                                                                                                            Query Match
                                                                                          SEQUENCE
                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                CATA_PSEAE
                                                                                                                                                                                                                                                                                            RESULT
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DD4CD
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                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-i- COFACTOR: HEME GROUP (BY SIMILARITY).
-i- SUBGUILIAR LOCATION: PEROXISOMAL and 91yoxysomal (By similarity).
-i- SUBCELLULAR LOCATION: PEROXISOMAL and 91yoxysomal (By similarity).
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                          RRFADSLGHPKVSQ -> KAIRRLARTPQRQP (IN
                                                                                                                                                                                                                                                                                                                                ö
V -> E (IN REF. 2).
AL -> R (IN REF. 2; AAA33441).
AL -> R (IN REF. 2).
MISSING (IN REF. 2).
A -> AE (IN REF. 2).
D -> AQ (IN REF. 2).
E -> Q (IN REF. 2; AAA33441).
                                                                                                                                                         F -> L (IN REF. 2).
PLRQAAP -> RRCGRAA (IN REF. 2).
                                                                                                                                                                                                                                                                                           Score 82; DB 1; Length 496;
Pred. No. 9.2e-05;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                           566FFD05B3795B49 CRC64;
                                                                                                                                          (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                         REF. 2).
C -> V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494 AA
                                                                                                                                          G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                       AH ->
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00199; catalase; 1.
PRINTS: PR00067; CATALASE.
ProDom: PD000510; Catalase; 1.
PROSITE: PS00431; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00432; 4BLC.
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                            56796 MW;
                                                                                                                                                                                                                                                                                                                                                              9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                            52.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U20778; AAA96948.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare (Barley).
                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                     245
254
264
264
281
282
319
319
319
408
                                                                                                                                                                                                                                            496 AA;
                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4513;
   2334
2234
2254
2264
2282
2382
3313
402
402
402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAT2_HORVU
P55308;
   CONFLICT
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CAT2_HORVU
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Rowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Howell M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ma J. F., Ochsner U.A., Klotz M.G., Nanayakkara V.K., Howell M. Johnson Z., Posey J.E., Vasil M.L., Monaco J.J., Hassett D.J., Saterioferritin A modulates catalase A (KatA) activity and resistance to hydrogen peroxide in Pseudomonas aeruginosa."; J. Bacteriol. 181:3730-3742(1999).
                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
   Length 494;
                                                                    Indels
Match 50.0%; Score 78.5; DB 1; Local Similarity 57.7%; Pred. No. 0.00031; les 15; Conservative 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   482 AA
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                 5 DVKQTTA-FGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99296583; PubMed-10368148;
                                                                                                                                                                                               13 DTKTTTTNAGOPVWNDNEALTVGPRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF047025; AAC03118.1; -. EMBL; AE004841; AAG07624.1; -.
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, La
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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us-09-488-737-2.rsp

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ACT_SITE
ACT_SITE
BINDING
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Best Local S
Matches 13
                                                                                                               RESULT 10
CAT1_GOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                Schmidt M.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEROXIDE.
-!- CATALITIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-!- CORACTOR: HERME GROUP.
-!- SUBGINIT: HOWOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Trititoeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

D725C042259AE494 CRC64;
                                                                                                              SIMILARITY).
                                                                                                                                                                                ö
         Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.; 1.
PROSITE; PS00438; CATALASE.2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                         ; Db 1,
.. 0.00036;
'.. 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1
PRONTOS; PR00067; CATALASE:
PROSTE; PS00437; CATALASE_1:
PROSTE; PS00437; CATALASE_1: 1
PROSTE; PS00438; CATALASE_1: 1
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                       Score 78; DB 1; Length 482
Pred. No. 0.00036;
                                                                                      BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY 6

84E5ABA647CAB414 CRC64;
                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
catalase (Rcl. 11.1.6).
Secale cereale (Rye).
                                                                                                                                                                                                                                                                                492 AA.
                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               2 VNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                      55 BY
128 BY
338 PF
55589 MW;
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. HALO; TISSUE-Leaf;
                                                                                                                                                       49.7%;
ilarity 57.1%;
Conservative
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                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yoxysome
                                                                                                                     482 AA;
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492 AA;
                                                                                                                                                                    Best Local Similarity
                                                                          Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                       55
128
338
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4550;
                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                             CATA_SECCE
P55310;
                                                                                                ACT_SITE
BINDING
SEQUENCE
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BINDING
                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                        RESULT 9
CATA_SECCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gossypium hirsutum (Upland cotton).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEROXIDE.
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-!- CORACTOR: HERE GROUP.
-!- SUBBNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: Peroxisomal.
-!- SUBCELLULAR LOCATION: PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

64886966A035F261 CRC64;
                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NI W., Turley R.B., Trelease R.N.;
"Characterization of a cDNA encoding cottonseed catalase.";
Biochim. Biophys. Acta 1049:219-221/1990.
-1- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00432, 4BEC.

InterPro; IPR00226; Catalase.

Pfam; PF00199; catalase, 1.

PRINTS; PR00067; Catalase; 1.

ProDom; PD00510; Catalase; 1.

PROSITE; PS00437; CATALASE.

PROSITE; PS00433; CATALASE.2; 1.

Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Peroxisome; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cch 48.4%; Score 76; DB 1; Length 492; 11 Similarity 61.9%; Pred. No. 0.00074; 13; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
  Score 77.5; DB 1,
Pred. No. 0.00044;
2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Catalase isozyme 1 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                     492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. DELTAPINE 62; TISSUE-Cotyledon;
MEDLINE-90304227; PubMed-2364113;
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                29
                                                                                                                                                 DVKQTTAF-GAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X52135; CAA36380.1; -. PIR; S10770; S10770. PIR; S10395; S10395.
     49.48;
Query Match
Best Local Similarity 57.73
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56855
                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAT1 OR SU1
                                                                                                                                                                                                                                                                                                                     CAT1_GOSHI
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SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                          thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                          pumpkin.";
Plant Mol. Biol. 33:141-155(1997).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                             Cucurbita pepo (Vegetable marrow) (Summer squash).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-!- COFACTOR: HEME GROUP (BY SIMILARITY).
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: GLYOXYSOMA1.
-!- TISSUE SPECIFICITY: HIGH EXPRESSION IN SEEDS AND EARLY SEEDLINGS.
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                              Esaka M., Yamada N., Kitabayashi M., Setoguchi Y., Tsugeki R.,
Kondo M., Nishimura M.;
"CDNA cloning and differential gene expression of three catalases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOm; PD000510; CATALASE.
PROSITE; PS00437; CATALASE.1:
PROSITE; PS00438; CATALASE.1: 1.
PROSITE; PS00438; CATALASE.2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75; DB 1; Length 492;
Pred. No. 0.001;
4; Mismatches 4; Indels
                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Catalase isozyme 1 (EC 1.11.1.6).
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                                                                                       492 AA
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                                                                                                                                                                                                                                                                                                                  MEDLINE-97188581; PubMed-9037166;
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ACT_SITE 65 65
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Local Similarity 61.9%;
Les 13; Conservative
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348 3
492 AA;
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                                                                                    CAT1_CUCPE
P48350;
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BINDING
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Matches
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                                                                         CAT1_CUCPE
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core eudicots; Rosidae;
                                                                              Embryophyta; Tracheophyta;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. LANDSBERG ERECTA;
Zentgraf U., Zinkernagel I.;
"A gene encoding a catalase isoform from Arabidopsis thaliana.";
                                                                                                                                                         Chevalier C., Yamaguchi J., McCourt P.; "Nucleotide sequence of a cDNA for catalase from Arabidopsis
P25819; 049615;
01-MAY-1992 (Rel. 22, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase 2 (EC 1.11.1.6).
CAT2 OR CAT OR AT4G35090 OR M4E13.140.
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudloctyledons; core eucrosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                           (In) Plant Gene Register PGR96-005.
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Plant Mol. Biol. 29:1005-1014(1995).
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492 AA; 56586 MW;
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61.9%;
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Triticum aestivum (Wheat).
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Best Local Similarity
Matches 13; Conserva
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                                                                                 PEROXIDE.
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ID CAT2_WHEAT
AC P55313;
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BINDING
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                                  SERVES
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-> L (IN REF. 1).

-> A (IN REF. 1).

-> I (IN REF. 1).

-> L (IN REF. 1).

-> L (IN REF. 1).

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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MEDLINE=96145511; PubMed=8555444;

Skadsen R.W., Schulze-Lefert P., Herbst J.M.;

"Molecular cloning, characterization and expression analysis of two

catalase isozyme genes in barley.";
                                                                                                                   -i-SUBUNIT: HOMOTETRAMER AND HETEROTETRAMER. AT LEAST SIX OR SEVEN ISOZYMES ARE PRODUCED FROM A MIXTURE OF 3 GENE PRODUCTS.
-i-SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal.
-i-SIMILARITY: BELONGS TO THE CATALASE FAMILY.
Nature 402:769-777(1999).

-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; S
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.

-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 1;
Pred. No. 0.001;
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Last annotation update)
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P55307; Q43761;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequestion of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG 29
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138
348
421
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!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                           -!- COFACTOR: HEME GROUP (BY SIMILARITY).
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
-!- TISSUE SPECIFICITY: IN WHOLE ENDOSPERMS (ALEURONES PLUS STARCHY ENDOSPERM), IN ISOLATED ALEURONES AND IN DEVELOPING SEEDS.
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
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-!- SUBUNIT: HOWOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: PELOXISOMAL and Glyoxysomal (By similarity).
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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ACT_SITE 65 BY SIMILARITY.
ACT_SITE 138 BY SIMILARITY.
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                                                                                                                     -!- CATALYTIC ACTIVITY: 2 \text{ H}(2)\text{O}(2) = \text{O}(2) + 2 \text{ H}(2)\text{O}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
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Pred. No. 0.0015;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Catalase (EC 1.11.1.6).
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Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.; 1.
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HSSP; P00432;
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CATA_PHAAU
ID CATA_PHAAU
AC P32290;
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ACT_SITE
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Gatalase from strictly anaerobic bacteria, Desulfovibrio vulgaris
(Miyazaki F).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROXIMAL HEME LIGAND (BY SIMILARITY). CFAED23345ED3C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; S
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-i- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-i- COFACTOR: HEME GROUP.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                    HSSP; P00432; 4BLC.
InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; P000510; CATALASE.
ProDom; PS00437; CATALASE.
PROSITE; PS00438; CATALASE.
PROSITE; PS00438; CATALASE.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desulfovibrio vulgaris (strain Miyazaki).
Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 1;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                           138 138 B
348 348 P
492 AA; 56480 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P42321; 2CAE.
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 TINSGAPVWNNNALTVGHRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.18;
61.98;
                                                                                                                                                                               EMBL; X94352; CAA64077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 Peroxisome; Glyoxysome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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Q9ZN99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KATA OR KAT
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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CATA_DESVM
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Matches
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Eukaryota; Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

NCBI_TaxID=3916;
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BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

933E604D2611CE85 CRC64;
                                                                SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BEDLINE-24151449; PubMed-8108520;
MOTİ H., Imasekî H.;
"CDNA for catalase from etiolated mung bean (Vigna radiata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73; DB 1; Length 492;
Pred. No. 0.0021;
                                                                                                                                                 Score 73; DB 1; Length 479;
Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide
  Hydrogen peroxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                           6; Indels
                    BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY
4CD97480AB6FD475 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                         492 AA
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                                                                                                                                                                                           2; Mismatches
Oxidoreductase; Peroxidase; Iron; Heme;
ACT_SITE 54 54 BY SIMILARI
ACT_SITE 127 BY SIMILARI
BINDING 337 337 PROXIMAL HE
SEQUENCE 479 AA; 54549 MW; 4CD97480A
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Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
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61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D13557; BAA02755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG
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Best Local Similarity 61.99
                                                                                                                                                   Query Match 46.5
Best Local Similarity 65.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peroxisome; Glyoxysome
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                                                                                                                                                                                                                                                                                                                                                                                                                            OXYGEN; SERVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                             STRAIN=168 / YB886;
MEDLINE=92097949; PubMed=1756979;
Bol D.K., Yasbin R.E.;
"The isolation, cloning and identification of a vegetative catalase gene from Bacillus subtills.";
Gene 109:31-37(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- DEVELOPMENTAL STAGE: ELEVATED LEVELS OF EXPRESSION DURING ENTRY INTO THE STATIONARY PHASE OF THE GROWTH CYCLE.
-i- INDUCTION: BY HYDROGEN PEROXIDE.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
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R EMBL; Z82044; CAB04807.1; -.
R EMBL; Z99108; CAB12710.1; -.
R PIR; JH0532; JH0532.
HSSP; P00432; 4BLC.
R SUbtilist; BG10849; katA.
R InterPro; IPR002226; Catalase.
R PRINTS; PR00067; CATALASE.
R PRODOM; P00006710; Catalase; 1.
R PROSITE; PS00437; CATALASE.
R PROSITE; PS00437; CATALASE.
R PROSITE; PS00438; CATALASE.
                                                                                                                                                                                                                                            Cummings N.J., Connerton I.F.; "The Bacillus subtilis 168 chromosome from sspE to katA."; Microbiology 143:1855-1859(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.2%; Score 71; DB 1; Length 482; 60.9%; Pred. No. 0.0041; iive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G -> P (IN REF. 1).
G -> D (IN REF. 1).
749F7C88CEA2E047 CRC64;
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BY SIMILARITY.
PROXIMAL HEME LIGAND
Bacteria; Firmicutes; Bacillus/Clostridium group;
                Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                             MEDLINE=97346037; PubMed=9202460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KOTTAFGAPVWDDNNVITAGPRG 29
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Best Local Similarity 60.9
Matches 14; Conservative
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53
126
336
205
372
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INIT_MET 0
ACT_SITE 53
ACT_SITE 126 1
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                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             [3]
SEQUENCE OF 1-18.
                                NCBI_TaxID=1423;
                                                                                                                                                                                                               STRAIN-168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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2A27C4BEC47BE854 CRC64;
                                                                                                                                                                                                                                                                                                                                                   "Purification, characterization and primary structure of a monofunctional catalase from Methanosarcina barkeri."; monofunctional catalase from Methanosarcina barkeri."; submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; S TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.

-i- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.

-i- COPACTOR: HEME GROUP (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN-FUSARO / DSM 804;
Shima S., Netrusov A., Sordel M., Wicke M., Hartmann G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
ACT_SITE 58 58 BY SIMILARITY.
ACT_SITE 131 131 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.9%; Score 72; DB 1; Length 505; 66.7%; Pred. No. 0.0031;
Live 1; Mismatches 6; Indels
                                                                                                          093662;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PETS BACSU STANDARD; PRT; 482 AA. P26901; P77838; 01-AUG-1992 (Rel. 23, Created) D-EMG-1998 (Rel. 37, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) Vegetative catalase (EC 1.11.1.6). Bacillus subtilis.
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P04040; 10QW.
InterPro; 1PR002226; Catalase.
Pfam; PPF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; P0000310; Catalase; 1.
PROSITE; PS00437; CATALASE.1: 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ005939; CAA06774.1; -.
|| ||||||||:||| :|| || || || TINSGAPVWNNNSLIVGIRG 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.73
Matches 14; Conservative
                                                                                            STANDARD;
                                                                                                                                                                                                            Methanosarcina barkeri.
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505 AA;
                                                                                                                                                                                                                                                             NCBI_TaxID=2208;
                                                                                                                                                                                                                                            Methanosarcina
                                                                                            CATA_METBA
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                                                                             CATA_METBA
             18
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Thu, Aug 22 08:03:52 2002

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AMEDLINE=21396507; PubMed=11481430;

A MEDLINE=21396507; PubMed=11481430;

A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

B Oistard P., Becker A., Boutry M., Cadiou E., Dreamo S., Gloux S.,

A Godie T., Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D.,

A Renard C., Tebault P., Vandenbol M., Weidher S., Gallbert F.;

A Renard C., Tebault P., Vandenbol M., Weidher S., Gallbert F.;

A Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:98779882(2001).

C I- FONCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES

C I- FONCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER CATIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.

C COPACTOR: HEME GROUP.

C I- SUBCELLULAR LOCATION: Periplasmic.

C I- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
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YCGCGSNPPSGSSPFVPASFFVPAEGTAEPRCGGVSSPRSR
AGFSPRIRALISSPVSVSYSSKPSARAT (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herouart D., Signud S., Moreau S., Frendo P., Touati D., Puppo A.; "Cloning and characterization of the katA gene of Rhizobium meliloti encoding a hydrogen peroxide-inducible catalase."; J. Bacteriol. 178:6802-6809(1996). SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase A (EC 1.11.1.6).
KATA OR R00764 OR SM000819.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
ProDom; PR00067; CATALASE.
ProDom; P0000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; FALSE_NEG.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 494;
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Pred. No. 0.0042;
                                                                                                                                                                  494 AA.
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-RCR2011 / SU47;
MEDLINE-97113440; PubMed-8955300;
KLTTSWGAPVGDNQNSMTAGSRG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
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P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Sinorhizobium NCBI_TaxID-382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U59271; AAC44649.1;
                                                                                                                                                                  STANDARD;
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                                                                                                                                                       CATA_RHIME P95631;
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Best Local Similarity

Query Match

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                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXYGEN; SERVES PEROXIDE.
 Gaps
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PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. W648; TISSUE-Leaf; WEDLINE-94035156; PubMed-8220459; WEDLINE-94035156; PubMed-8220459; Guan L., Scandalios JG.; The catalase antioxidant defense gene Catl of "Characterization of the catalase antioxidant defense gene Catl of maize, and its developmentally regulated expression in transgenic
                                                                                                                                                                                                                                                                                                           STRAIN=CV. R6-67; TISSUE-Scutellum;
MEDLINE-89051000; PubMed-2461221;
Redinbaugh M.G., Wadsworth G.J., Scandalios J.G.;
"Characterization of catalase transcripts and their differential expression in maize.";
Biochim. Biophys. Acta 951:104-116(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_1; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
Peroxisome; Multigene family.
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> V (IN STRAIN W64A)
 5,
                                                                                                                                             01-NoV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
catalase isozyme 1 (EC 1.11.1.6).
                                                                                                                      492 AA
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 Mismatches
                                                                                                                       PRT;
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                          9 TTAFGAPVWDDNNVITAGPRG 29
                                                 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X12538; CAA31056.1; -. EMBL; X60135; CAA42720.1; -. PIR; JA0090; JA0090. HSSP; P21179; ICF9.
                                        14; Conservative
                                                                                                                       STANDARD;
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138
348
157
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   NCBI_TaxID=4577;
                                                                                                                                                                                                                  Zea mays (Maize)
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                                                                                                                      CAT1_MAIZE
P18122;
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BINDING
VARIANT
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                                                                                           RESULT 20
CAT1_MAIZE
  Matches
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Indels

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12; Conservative
     Best Local Similarity
                                                                                                                                   RESULT 22
CAT1_ARATH
                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. NIPPONBARE;
MEDLINE=94336766; PubMed=8058828;
MEDLINE=94336766; PubMed=8058828;
MOTIAE S., Tasaka M., Fujlsawa H., Ushimaru T., Tsuji H.;
A CDNA clone encoding a rice catalase isozyme.";
Plant Physiol. 105:1015-1016(1994).
I-FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
I-CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
I-CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
I-SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
I-SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
I-SUBCELLULAR LOCATION: DELOXISOMAL and glyoxysomal (By similarity).
I-SUBLIBARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROXIMAL HEME LIGAND (BY SIMILARITY). 08963B05BA6C20AB CRC64;
                                                                                                                                                                                     ;
                                                                                                                                                      Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                   5; Indels
S -> T (IN STRAIN W64A).
P -> I (IN STRAIN W64A).
P -> A (IN STRAIN W64A).
A -> G (IN REF. 1).
C -> G (IN REF. 1).
C -> D (IN REF. 1).
C -> D (IN REF. 1).
                                                                                                                                                  44.6%; Score 70; DB 1; 57.1%; Pred. No. 0.0059;
                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Catalase isozyme B (EC 1.11.1.6) (CAT-B).
                                                                                                                                                                                                                                                                                                                                    492 AA
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PEROXISOME: MILLIGHE FAMILY.
ACT_SITE 65 BY SIMILARITY.
ACT_SITE 138 138 BY SIMILARITY.
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR00226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
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                                                                                                                                                                                                                                       18 TTNSGAPVWNNNSALTVGQRG 38
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                                                                                                    56877
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
 211
329
483
332
415
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492 AA;
                                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                    492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
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                                                  CONFLICT
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                                  VARIANT
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CATB_ORYSA
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DB 1; Length 492;

44.6%; Score 70;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                    Gaps
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-!- COFACTOR: HEME GROUP.
-!- SUBUNIT: HOMOTETRAMER AND HETEROTETRAMER. AT LEAST SIX OR SEVEN
-!- SUBUNIT: HOMOTETRAMER PROM A MIXTURE OF 3 GENE PRODUCTS.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. Columbia;
MEDLINE-98250696; PubMed-9584109;
RIUGOLI J.A., McPeek M.A., Thomas T.L., McClung C.R.;
Firtyon loss and gain during evolution of the catalase gene family anglosperms.;
Genetics 149:355-365(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frugoli J.A., Zhong H.H., Nuccio M.L., McCourt P., McPeek M.A., Thomas T.L., McClung C.R.; Cartalase is encoded by a multigene family in Arabidopsis thaliana (L.) Heynh.";
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BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

G -> E (IN REF. 1).

G -> F (IN REF. 1).
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HSSP, P00432; 4BLC.

RICHARD PP00192; catalase.

PFdam; PP00105; catalase; 1.

PRINTS; P800065; CATALASE.

PRODOM; PD000510; CATALASE.1.

PROSITE; PS00437; CATALASE.2; 1.

PROSITE; PS00438; CATALASE.2; 1.

Whiltigene family.

ACT_SITE 65 65 BY SIMILARITY.

ACT_SITE 138 138 BY SIMILARITY.

PACT_SITE 138 138 PROXIMAL HEME LIGAND (BY SIMILARI CONFLICT 103 103 F -> E (IN REF. 1).
Pred. No. 0.0059;
                                                                                                                                                                                                   CATI_ARATH STANDARD; PRT; 492 AA. 096528; 022529; 01-NOV-1997 (Rel. 35, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) catalase 1 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. LANDSBERG ERECTA;
MEDLINE-96416445; Pubmed-8819328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Physiol. 112:327-336(1996).
                                                                       29
                                                                                              18 TINSGAPVWNNNSALTVGERG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF021937; AAC17731.1;
                                                                       9 TTAFGAPVWDDNNVITAGPRG
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Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.
-:- COFACTOR: HEME GROUP.
-:- SUBGULT: HOMOTETRAMER.
-:- SUBCLIGILAR LOCATION: Peroxisomal and glyoxysomal (Potential).
-:- TISSUE SPECIFICITY: ABUNDANT IN ENDOSPERMS AND COTYLEDONS. ONLY IN SMALL AMOUNT IN ROOT.
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glyoxysomal targeting sequence.";
Eur. J. BLOchem. 199:1215(1991).
-!- EUNCTION: OCCURS IN ALMOST ALLA BROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLE FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Stróptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Hypocotyl;
MEDLINE-94325474; PubMed-8049373;
Suzuki M., Ario T., Hattori T., Nakamura K., Asahi T.;
Isolation and characterization of two tightly linked catalase genes from castor bean that are differentially regulated.";
Plant Mol. Biol. 25:507-516(1994).
                                                                                                                                                      Gaps
                                                                                                                                                    ;
0
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                                                                                                            Length 492;
                                                                                                                                                    5; Indels
  L -> NV (IN REF. 1).
-> W (IN REF. 1).
370F54FF7D757C9B CRC64;
                                                                                                          DB 1;
0.012;
                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                              492 AA
                                                                                                                                                    Mismatches
                                                                                                          Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                            PRT;
    KL -> S
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01-FEB-1996 (Rel. 33, Last sequenc
01-FEB-1996 (Rel. 33, Last annota!
Catalase isozyme 1 (EC 1.11.1.6).
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MEDLINE-91293125; PubMed-1712298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR002226; Catalase.
Pfam: PF00199; Catalase; 1.
PRINTS: PR00067; CATALASE.
PRODOM: PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricinus communis (Castor bean).
                                                                                                                                                    4;
                                            56861 MW;
                                                                                                                                                                                            9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                  SEQUENCE OF 404-492 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D21161; BAA04697.1; -. EMBL; X59694; CAA42215.1; -.
                                                                                                      cch 43.3%;
al Similarity 57.1%;
12; Conservative
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  340
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PIR; S29333; S29333.
HSSP; P21179; 1CF9.
339 3
455 4
492 AA;
                                                                                                        Query Match
Best Local Similarity
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CONFLICT
CONFLICT
SEQUENCE
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CAT1_RI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ni W., Trelease R.N.;
"Two genes encode the two subunits of cottonseed catalase.";
Arch. Biochem. Biophys. 289:237-243(1991).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PRONCINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
Peroxisome; Glyoxysome; Multigene family.
ACT_SITE 65 65 BY SIMILARITY.
ACT_SITE 138 138 BY SIMILARITY.
BY SIMILARITY.
THE 138 348 PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-!- COFACTOR: HEME GROUP.
-!- SUBURIT: HOMOTETRAMER.
-!- SUBCELLUAR LOCATION: Peroxisomal.
-!- SUBCELLUAR LOCATION: PEROXISOMAL.
-!- MISCELLANEOUS: THERE ARE AT LEAST FIVE ISOZYMES OF CATALASE IN
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                       Score 68; DB 1; Length 492;
Pred. No. 0.012;
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                                                                                                                                                                                                                                             -> Q (IN REF. 2).
B5E28A425088BF63 CRC64;
                                                                                                                                                  A -> P (IN REF. 2).
F -> S (IN REF. 2).
L -> F (IN REF. 2).
D -> E (IN REF. 2).
H -> Q (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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STRAIN=CV. DELTAPINE 62; TISSUE-COLYledon;
MEDLINE-91378551; PubMed-1898069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gossypium hirsutum (Upland cotton)
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PRODOM; PD009510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
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Pfam; PF00199; catalase; 1.
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Μ
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                                                                                                                                                                                                                                                                        56464
                                                                                                                                                                                                                                                                                                                                          Query Match 43.3
Best Local Similarity 57.1
Matches 12; Conservative
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348
4439
4454
456
                                                                                HSSP; P00432; 4BLC
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01-APR-1993
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CAT2_GOSHI
ID CAT2_GOSHI
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TISSUE-Leaf
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Q59714;
                                   CATA_PEA
P25890;
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BINDING
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                                                                                                                                                                                                                                                                                       Gaps
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               BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
589FD8DCA173AB12 CRC64;
                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Primulaceae; Soldanella.
NCBI_TaxID=66308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COXIMAL HEME LIGAND (BY SIMILARITY). OCC8A9B2597A9EEA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.3%; Score 68; DB 1; Length 492; 57.1%; Pred. No. 0.012;
                                                             Length 492;
                                                                                5; Indels
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                                                             43.3%; Score 68; DB 1; 57.1%; Pred. No. 0.012;
                                                                                                                                                                              01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase (EC 1.11.1.6).
Soldanella alpina (Alpine snowbell).
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BY SIMILARITY.
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PROXIMAL HEME
                                                                                Mismatches
         SIMILARITY
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Ffam; PF00199; Catalase: 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase: 1.
PROSITE; PS00431; CATALASE 1: 1.
PROSITE; PS00438; CATALASE 2: 1.
Oxidoreductase; Peroxidase; Iron;
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                                   56935 MW;
                                                                                                  9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                           56921 MW;
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Multigene family.
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                                                                                Conservative
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492 AA;
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12; Conserv
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Best Local Similarity
Matches 12; Conserv
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SEQUENCE FROM N.A.
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Peroxisome;
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                                                                                                                                                               CATA_SOLAP
024339;
        ACT_SITE
ACT_SITE
BINDING
                                   SEQUENCE
                                                              Query Match
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18 TINSGAPVWNNNSSLIVGTRG 38

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                                                                                                                                                                                                                                                                                                                                                                             Isin S.H., Allen R.D.;
"Isolation and characterization of a pea catalase cDNA.";
Plant Mol. Biol. 17:1263-1265(1991).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                    Pisum sativum (Garden pea).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O. COFACTOR: HEME GROUP.
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PROXIMAL HEME LIGAND
B5FC08E66B13B266 CR
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-1- SUBCELLULAR LOCATION: Peroxisomal.
-1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.3%; Score 68; DB 1; ilarity 57.1%; Pred. No. 0.012; Conservative 4; Mismatches
                                             01-MAY 1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Catalase (EC 1.11.15).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Catalase (EC 1.11.1.6).
494 AA.
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BY SIMILARITY.
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PIR; S18346; CSPM.
HSSP; PO0432; 4BLC.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PROSITE; PS00437; CATALASE.
PROSITE; PS00438; CATALASE.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92032793; PubMed=1932700;
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57344 MW;
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  STANDARD;
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494 AA;
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Best Local Similarity
Matches 12; Conserv
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                                           SEQUENCE FROM N.A.
STRAIN=CV. CORSOY 79;
Su H., Hardy K.A., Hermsmeier D., Baum T.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                      -:- COFACTOR: HEME GROUP.
-:- SUBUNIT: HOMOTETRAMER.
-:- SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Willekens H., Villarroel R., van Montagu M., Inze D., van Camp W.; "Molecular identification of catalases from Nicotiana plumbaginifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROXIMAL HEME LIGAND (BY SIMILARITY). CE8AFE8BEEA483C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB 1; Length 492;
Pred. No. 0.017;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana
NCBI_TaxID=4092;
                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Catalase isozyme 3 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; reloximos, percentidanily.
Percoxisome; Glyoxysome; Multigene family.
65 BY SIMILARITY.
7. THE 138 BY SIMILARITY.
Plant Mol. Biol. 17:1263-1265(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Flower;
MEDLINE-95010681; Pubmed-7925949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR002226; Catalase.
Pfam, PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035252; AAB88169.1; -. EMBL; AF035253; AAB88170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56847 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 TTNSGAPIWNNNSSLTVGSRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z12021; CAA78056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.78;
52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett. 352:79-83(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
138
348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S20999; CSSY.
HSSP; P21179; 1CF9
                                                                                                                                                                               PEROXIDE.
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ID CAT3_NICPL
AC P49317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                  putida.";
Gene 199:219-224(1997).
-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE.
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROXIMAL HEME LIGAND (BY SIMILARITY).
EFE3CBDE67778571 CRC64;
                                                                                                                                                                                                    Kim Y.C., Miller C.D., Anderson A.J.;
"Identification of adjacent genes encoding the major catalase and
bacterioferritin from the plant-beneficial bacterium Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                       Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.7%; Score 67; DB 1; Length 479; llarity 66.7%; Pred. No. 0.016; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. D&PL 415;
MEDLINE-92032793; PubMed=1932700;
Isin S.H., Allen R.D.;
"Isolation and characterization of a pea catalase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide
                                                                                                                                                                                                                                                                                                                                                                            -i- COFACTOR: HEME GROUP.
-i- ENZYME REGULATION: ACTIVATED BY PEROXIDE.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
CATI AND CAT2.
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BY SIMILARITY
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                                                                                                                                                                               MEDLINE-98019091; PubMed-9358059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002226; Catalase.
Pfam: PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U63511; AAB88219.1; -. HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                             STRAIN-CORVALLIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3847;
                                                                                          NCBI_TaxID=303;
    OR CATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAT1_SOYBN P29756;
                                                                     Pseudomonas
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Best Local Sim
Matches 14;
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CAT1_SOYBN

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Gaps

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PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                CAT4_SOYBN 048561;
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                                                                                                                                                                                                                                                              Matches
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 OXYGEN; SERVES PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-1- COFACTOR: HEME GROUP.
-1- SUBGELILIA: HOMOTETRAMER (By similarity).
-1- SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
-1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Eabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                             PROXIMAL HEME LIGAND (BY SIMILARITY).
2A49AD89CC6FB4D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                          InterPro: 1PR00226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Peroxisome; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN -!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O. -!- COFACTOR: HEME GROUP. -!- SUBGRILLARITY). -!- SUBCELLIAR LOCATION: Peroxisomal (Potential). -!- INDUCTION: BY 3-AMINOTRIAZOBE.
                                                                             -! - SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 1;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase 3 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  492 AA
                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                        492 AA; 57016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                 18 TTNSGAPVWNNNSSMTVGTRG 38
                                                                                                                                                                                                                                                                                                                                                                         42.7%;
57.1%;
                                                                                                                                                                                        EMBL; Z36977; CAA85426.1; -. HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (Soybean)
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAT3_SOYBN
O48560;
01-MAR-2002 (
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                                                                                                                                                                                                                                                                                                                 ACT_SITE
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
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EMBL; AF035254; AAbc...

DR HSSP; P21179; 1CF9.

InterPro; PR002226; Catalase.

DR Pfum; PF00199; Catalase; 1.

DR PF00199; Catalase; 1.

DR PROSTE; PS00437; CATALASE.

DR PROSTE; PS00437; CATALASE.1; 1.

DR PROSTE; PS00438; CATALASE.2; 1.

KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;

KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;

KW Oxidoreductase; Beroxidase; Iron; Heme; Hydrogen peroxide;

KW ACT_SITE 65 65 BY SIMILARITY.

ACT_SITE 65 65 BY SIMILARITY.

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Su H., Hardy K.A., Hermsmeier D., Baum T.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ARROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-i- COFACTOR: HEME GROUP.
-i- SUBUNIT: HOMOTETRAMER (By similarity).
-i- SUBCELLULAR LOCATION: PELOXISOMAl and 91yoxysomal (By similarity).
-i- SUBCELLULAR LOCATION: TO THE CATALASE FAMILY.
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Bukaryophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase 4 (EC 1.11.1.6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002226; Catalase.
Pfam: PF00199; Catalase; 1.
PRINTE; PR00067; CATALASE.
PRODOM: PD00010; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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DB 1;
0.024;
                                                                                                                                                                                                                     01-NOV-1986 (Rel. 03, Created)
16-02T-2001 (Rel. 40, Last sequence update)
18-1-1-2002 (Rel. 41, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of human erythrocyte catalase.";
Acta Crystallogr. D 56:241-245(2000).
                                                                                                                                                                                       526 AA
                                   Mismatches
 Score 66;
Pred. No.
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Fibroblast;
MEDLINE-85054813; PubMed-6548744;
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86286565; PubMed-375556;
                                 .
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                                                                   9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                       || | |: | |::||||||
TTGSGNPIGDKLNILTAGPRG 47
 42.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 76-526 FROM N.A.
Query Match 42.0
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abraham D.J.;
                                                                                                                                                                       CATA_HUMAN
ID CATA_HUMAN
                                                                                                                                                                                                         P04040;
                                                                                                   27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics. The Flutte. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-LANDRACE; TISSUE-Liver;

MEDILINE-9913641; PubMed-9475954;

Lin Z.-H., Wang Y.-F., Sarai A., Yasue H.;

Lin Z.-H., Wang Y.-F., Sarai A., Yasue H.;

Swine catalase deduced from cDNA and localization of the catalase gene on swine chromosome 2p16-p15.";

Biochem. Genet. 35:297:302(1997).

-!- FUNCTION: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LICAND (BY SIMILARITY).
                                                                                   PROXIMAL HEME LIGAND (BY SIMILARITY). FEF3B4706A4FD669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00432; 4BLC.
InterPro: IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSTE; PS00437; CATALASE_1; 1.
PROSTE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
                                                                                                                                                                                         ö
                                                                                                                                                   42.7%; Score 67; DB 1; Length 492; llarity 52.4%; Pred. No. 0.017; Conservative 5; Mismatches 5; Indels
                   Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEROXIDE.
-1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-1- COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).
-1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-1- SUBCELLIAR LOCATION: PECOXISOMAI (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydi
Peroxisome; Glyoxysome; Multigene family.
ACT_SITE 65 BY SIMILARITY.
ACT_SITE 138 BY SIMILARITY.
BINDING 348 PROXIMAL HEME I
                                                                                                                                                                                                                                                                                                                                             502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57182 MW;
                                                                                                   492 AA; 56737 MW;
                                                                                                                                                                                                                         TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                           18 TINSGAPIWNNNSSLTVGARG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D89812; BAA25301.1; -.
                                                                                                                                                                                                                                                                                                                                              STANDARD;
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74
147
357
502 AA;
                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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INIT_MET
ACT_SITE
                                                                                                                                                                                                                                                                                                                                           CATA_PIG
062839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
BINDING
                                                                                                     SEQUENCE
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Gaps
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MEDLINE-20133173; PubMed-10666617;
KO T.P., Safo M.K., Musayev F.N., Di Salvo M.L., Wang C., Wu S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
MEDLINE=20124014; PubMed=10656833;
Putnam C.D., Arvai A.S., Bourne Y., Tainer J.A.;
"Active and inhibited human catalase structures: ligand and NADPH binding and catalytic mechanism.";
J. Mol. Biol. 296:295-309(2000).
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Korneluk R.G., Quan F., Lewis W.H., Guise K.S., Willard H.F., Holmes M.T., Gravel R.A.; Isolation of human fibroblast catalase CDNA clones. Sequence of clones derived from spliced and unspliced mRNA."; J. Biol. Chem. 259:13819-13823(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-21 FROM N.A. MEDILIBE-9110338; PubMed-9282800; MEDILIBE-9110338; PubMed-9282800; Voo J.-H., Erzurum S.C., Hay J.G., Lemarchand P., Crystal R.G.; "Vulnerability of the human airway epithelium to hyperoxia. Constitutive expression of the catalase gene in human bronchial epithelial cells despite oxidant stress."; J. Clin. Invest. 93:297-302(1994).
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MEDDLINE-8628646; Pubmed-3755225;
Quan F., Korneluk R.G., Tropak M.B., Gravel R.A.;
"Isolation and characterization of the human catalase gene.";
Nucleic Acids Res. 14:5321-5335(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                          Bell G.I., Najarian R.C., Mullenbach G.T., Hallewell R.A.; "cDNA sequence coding for human kidney catalase."; Nucleic Acids Res. 14:5561-5562(1986).
Length 502,
                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE-21065390; Pubmed=11134921;
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27 TTGAGNPVGDKLNVITVGPRG 47
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Safo M.K., Musayev F.N., Wu S.H., Abraham D.J., KO T.P.;
"Structure of tetragonal crystals of human erythrocyte catalase.";
Acta Crystallogr. D 57:1-7(2011).
-!- FUNCTION: OCCURS IN ALMOST HIL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                             -i-CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-i-COFACTOR: HEME GROUP AND NADP.
-i-SUBGUILLAR LOCATION: Peroxisomal.
-i-DISEASE: Deficiency in CAT causes acatalasia (or acatalasemia).
This disease is characteized by absence of catalase activity in red cells and is often associated with ulcerating oral lesions.
-i-SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS: PRO0009; Catalase; 1.
PRINTS: PRO0067; Catalase; 1.
PRODOM: PRO00510; Catalase; 1.
PROSITE; PS00437; CATALASE; 1.
PROSITE; PS00438; CATALASE_1; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROXIMAL HEME LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                  X04093; CAA27721.1; JOINED.
X04094; CAA27721.1; JOINED.
X04095; CAA27721.1; JOINED.
X04096; CAA27721.1; JOINED.
L13609; AAA16651.1;
                                                                                                                                                                                                                                                                                                                             X04088; CAA27721.1; JOINED.
X04089; CAA27721.1; JOINED.
X04090; CAA27721.1; JOINED.
                                                                                                                                                                                                                                                                                            X04085; CAA27721.1; -
X04086; CAA27721.1; JOINED.
X04087; CAA27721.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                               X04091; CAA27721.1; JOINED. X04092; CAA27721.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1F4J; 17-JAN-01.
SWISS-2DPAGE; P04040; HUMAN.
Aarhus/Ghent-2DPAGE; 1524; IEF.
Aarhus/Ghent-2DPAGE; 1525; IEF.
Aarhus/Ghent-2DPAGE; 1526; IEF.
                                                                                                                                                                                                                                                          EMBL; X04076; CAA27717.1; -.
EMBL; K02400; AAB59522.1; -.
EMBL; AL035079; CAB45236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peroxisome; NADP; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100W; 14-JUN-99.
1DGB; 11-FEB-00.
1DGF; 11-FEB-00.
1DGG; 17-FEB-00.
1DGH; 17-FEB-00.
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A23651.
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526 AA;
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A23646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A23651;
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                                                         PEROXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
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EMBL;
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EMBL;
EMBL;
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PDB;
PDB;
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PDB;
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PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Dacterium Bacteroides fragilis..;
-1. Bacterium. 177:3111.3119(1995).
-1. FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
MAY BE INVOLVED IN AEROTOLERANCE OF B. FRAGILIS.
-1. CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                  Bacteroides fragilis.
Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
                                                                                                                                                                                                                                                                                                                                              MEDLINE-95286491; PubMed-7768808;
Rocha E.R., Smith C.J.;
"Biochemical and genetic analyses of a catalase from the anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROXIMAL HEME LIGAND (BY SIMILARITY). 4F28A24ED9B9A966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: HOMODIMER.
-i- INDUCTION: UPREGULATED BY OXYGENATION AND STATIONARY PHASE.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.

ACT_SITE 54 54 BY SIMILARITY.

ACT_SITE 127 127 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.4%; Score 65; DB 1; Length 486; 55.2%; Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NNY-2000 (Rel. 39, Last annotation update)
Catalase (EC 1.11.1.6).
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.; 1.
PROSITE; PS00438; CATALASE.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002226; Catalase.
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55905 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U18676; AAC43384.1; -. HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 55.2
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
STANDARD:
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486 AA;
                                                                                                                                                                                                                                               NCBI_TaxID=817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATA_HAEIN
P44390;
01-NOV-1995 (
01-NOV-1995 (
16-OCT-2001 (
                                                                                                                                                  KATA OR KATB
                                                                                                                                                                                                                          Bacteroides
CATA_BACFR
P45737;
                                                                                                                                                                                                                                                                                                                            STRAIN=638
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ACT_SITE
BINDING
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Gaps

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42.0%; Score 66; DB 1; Length 526; 66.7%; Pred. No. 0.026; 7; Indels iive 0; Mismatches 7; Indels

9 TTAFGAPVWDDNNVITAGPRG 29

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Ouery Match
Best Local Similarity 66.79

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9 TTAFGAPVWDDNNVITAGPRG
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                                                                                                                                                       CATA_CANFA
                                                                                                                                                                                                       SOUTH THE TENT TO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERVES
                                                                                                                                                                                                                                               Bishai W.R., Smith H.O., Barcak G.J.;
"A peroxide/Ascorbate-inducible catalase from Haemophilus influenzae is homologous to the Escherichia coli katE gene product.";
J. Bacteriol. 176:2914-2921(1994).
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RD KWAND / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
UtterDack T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 269:496-512(1995).
--- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; S TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
--- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
Catalase (EC 1.11.1.6).
KATA OR HKTE OR H10928.
Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Hemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}.\,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
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N -> T (IN REF. 1).
N -> S (IN REF. 1).
N -> T (IN REF. 1).
4; 4FAFC16D844043B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - COFACTOR: HEME GROUP.
-i - SUBGNIT: HOMOHEXAMER (BY SIMILARITY).
-i - SUBGLILAR LOCATION: CYTOPLASMIC (Probable).
-i - INDUCTION: BY HYDROGEN PEROXIDE.
-i - SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-94245618; PubWed-8188593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0067; CATALASE.
Prodom; PRO0015; CATALASE; 1.
PROSITE; PSO0437; CATALASE_1; 1.
PROSITE; PSO0438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
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                                                                                                                                                                                                                                                                       "A peroxide/ascorbat
is homologous to the
J. Bacteriol. 176:29
[2]
SEQUENCE FROM N.A.
STRAIN=RD / KW20 / P
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357
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413
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508 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                      "cDNA sequence and deduced amino acid sequence of dog catalase.";
Submitted (APR-1998) to the EMBL/GenBank/DDDJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL BENOBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -: CATALTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-: COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).
-: SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-: SUBCELLIARN LOCCATION: PETCATSOMAI (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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llarity 61.9%; Pred. No. 0.037;
Conservative 2; Mismatches
                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
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BY SIMILARITY.
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB012918; BAA36420.1; -. HSSP; P00432; 4BLC.
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                                                                                                                                                                                                                                                                                                                                                   STRAIN-BEAGLE; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00199; catalase; 1
PRINTS; PR00067; CATALASE.
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STANDARD;
                                                                                                                                                                                    Canis familiaris (Dog).
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357
526 AA;
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                  Nakamura K.;
CATA_CANFA 097492;
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BINDING
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Gaps

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41.4%; Score 65; DB 1; Length 508; 61.9%; Pred. No. 0.035; ive 2; Mismatches 6; Indels

Conservative

Best Local Similarity Matches 13; Conserv

Query Match

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                                                                                                                                                                                Saruyama H., Matsumura T.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                             PEROXIDE.
-:- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-:- CORACTOR: HEME GROUP (BY SIMILARITY).
-:- SUBNIT: HOMOTERAMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                       Triticum aestivum (Wheat).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
Catalase (EC 1.11..6).
Helianthus annuus (Common sunflower).
Helianthus annuus (Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. SPANNERS ALLZWECK; TISSUE-Cotyledon;
MEDLINE-95101741; PubMed-7803505;
Kleff S., Trelease R.N., Eising R.;
"Nucleotide and deduced amino acid sequence of a putative higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intereto.
Pfam, PF00199; catalase.
PRIMTS; PR00065; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
Peroxisome; Glyoxysome; Multigene family.
Peroxisome; Glyoxysome; Multigene family.
BY SIMILARITY.
65 138 BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 0.048;
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InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
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52.48;
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    Catalase 1 (EC 1.11.1.6).
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                          NCBI_TaxID=4565;
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P45739;
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    g
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                                                                                                                                                                                                                                                                            STRAIN=HARTLEY; TISSUE=Lung;
MEDLINE=96180130; PubMed=8597602;
Yuan H.T., Bingle C.D., Kelly F.J.;
"Differential patterns of antioxidant enzyme mRNA expression in guinea pig lung and liver during development.";
Biochim. Biophys. Acte 1305:163-171(1996).
-!- FUNCTION: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC BFFECTS OF HYDROGEN
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                                                        Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP; Peroxisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                            Pinteric M., Baumgart E., Bulitta C., Fahimi D., Voelkl A.; "Molecular characterization of guinea pig catalase."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 526;
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7B58FDD76255E276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 1;
Pred. No. 0.037;
16-OCT-2001 (Rel. 40, Last annotation update) Catalase (EC 1.11.1.6).
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U39841; AAC52717.1; -. HSSP; P00432; 4BLC.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; I. PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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59802 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
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61.98;
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SEQUENCE OF 1-137 FROM N.A.
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357
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526 AA;
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Best Local Similarity
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                                                                                                                    NCBI_TaxID=10141;
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CAT1_WHEAT
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SIMILARITY).

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SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Peroxisomal (By similarity).
SIMILARITY: BELONGS TO THE CATALASE FAMILY.
     COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Job time: 158 sec
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                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] SEQUENCE FROM N.A.
Ken C.F., Lin C.T., Wu J.L., Shaw J.F.;
"Molecular cloning of a cDNA coding for catalase from zebrafish (Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comp. Blochem. Physiol. 127:447-457(2000).
-!-PUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                  SERVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerhard G.S., Kauffman E.J., Grundy M.A.;
"Molecular cloning and sequence analysis of the Danio rerio catalase
gene.";
molecular weight precursor for catalase in sunflower cotyledons.";
Blochim. Blophys. Acta 1224:463-466(1994).

Blochim. Blophys. Acta 1224:463-466(1994).

FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SER TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.

-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.

-!- COFACTOR: HEME GROUP.

-!- SUBGELLULAR LOCATION: PEROXISOMAL (By similarity).

-!- SUBCELLULAR LOCATION: PEROXISOMAL (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

4ASCS96S06F4496I CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cch 40.8%; Score 64; DB 1; Length 492; 11 Similarity 57.1%; Pred. No. 0.048; 12; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000510; Catalase; 1. PROSITE; PS00437; CATALASE_1; 1. PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                       InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    56755 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 TTNSGAPVYNNNNSLTVGSRG 38
                                                                                                                                                                                                                                                           EMBL; L28740; AAA69866.1; -. HSSP; P00432; 4BLC.
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492 AA;
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BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
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                                                                                                                                                                                             HSSP; P00432; 4BLC.

ZFIN; ZDB-GENE-000210-20; cat.
InterPro; IPR002205; Catalase.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00433; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
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Pred. No. 0.052;
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T -> I (IN REF. 2).
T -> I (IN REF. 2).
S -> F (IN REF. 2).
MIQ. -> NAAA (IN REF. 2).
M -> T (IN REF. 2).
W -> T (IN REF. 2).
W -> T (IN REF. 2).
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                                                                                                                                                              EMBL; AJ007505; CAB64949.1; -. EMBL; AF170069; AAF89686.1; -.
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Scoring table:

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Database

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AAM403117
AAM404314
AAY41121
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AAY71122
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AAY23609
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Helicobacter CP2 a
Helicobacter CP2-P
Helicobacter CP2-P
H. pylori GHPO 358
Helicobacter pylor
Helicobacter pylor
Arabidopsis thalia
Arabidopsis thalia
Clone of A. thalia
                                                                                                                                                                                                                                          A_Geneseq_032802:*

| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
                                                      August 22, 2002, 07:44:04; Search time 51.87 Seconds (without alignments) 62.100 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H.pylori catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                 the number of results predicted by chance to have a than or equal to the score of the result being printed, by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                          1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                    747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 100 summaries
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AAW06481
AAW06482
AAW98423
AAW54146
AAW52810
AAG23826
AAG23826
AAY18131
                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR88244
                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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157
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Human bone marrow
Peptide #305 enco
Peptide #305 enco
Peptide #305 enco
Peptide #306 enco
Peptide #3030 enco
Bacillus thermoglu
V. rumoiensis S-1
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AAW33405 standard; peptide; 29 AA.

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Candida albicans,
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Human polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                            The N-terminal sequence of the 54 kD monomeric subunit of the Helicobacter pylori ATCC 43579 catalase. The complete catalase (a tetrameric protein) can be used in compsns. for immunising against H.pylori, pref. those implicated in gastritis, peptic ulcers and stomach cancer. The compsns. contain inactive mutant forms of the catalase and may also contain adjuvants e.g. alum, and other H.pylori antigens e.g. urease. The compsns. are pref. encapsulated in liposomes.
                                                                                                                                                                                                                            Helicobacter pylori; catalase; immunisation; gastritis; peptic ulcer; stomach cancer; mutant; antigen; urease; encapsulate; liposome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                   Vaccines against Helicobacter pylori - contg. H. pylori catalase
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0
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100.0%; Pred. No. 6.8e-17;
ive 0; Mismatches 0;
                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                        (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
                                   AAM78945
AAM39546
AAG52458
AAG45660
                                                                                                     AAR75111
AAB92908
        AAG52460
                      AAG52459
                                                                 AAM79929
                                                                         AAM41332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                             AAG45661
                                                                                                                                                                   AAR88244 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 4; 14pp; French.
                                                                                                                                                                                                               H.pylori catalase N-terminus.
 95WO-FR00383,
                                                                                                                                                                                                                                                                                                          94FR-0004172
                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                  Helicobacter pylori.
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Matches 29; Conserv
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                                                                                                                                                                                               17-MAY-1996
                                                                                                                                                                                                                                                               W09527506-A1
                                                                                                                                                                                                                                                                                           27-MAR-1995;
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Lissolo L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Helicobacter pylori membrane proteins - and related polypeptide(s) and antibodies, useful for active or passive immunisation and diagnosis
                                                                                                                                               membrane protein; vaccine; immunisation; immunoassay;
diagnostic; affinity purification; gastritis; peptic ulcer;
gastric cancer.
                                                                                                N-terminal sequence of 54 kD membrane protein of H. pylori.
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100.0%; Pred. No. 6.8e-17;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
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                                                                                                                                                                                                                                                                                                                                                                                                         96WO-FR01552.
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                                              (first entry)
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                                                                                                                                                                                                                                                    Helicobacter pylori.
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 AA;
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AAW33405;
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Helicobacter pylori ATCC 43504 CP2 antigen (AAW06481) is useful in the specific and quantitative detection of H. pylori and in vaccine prodn. CP2 antibody titre shows high correlation with the pathology of gastritis. The CP2 amino acid sequence was deduced from a genomic clone (AAT45042). Slightly different sequences, CP2-PCR1 (AAW06482) and CP2-PCR2 (AAW06483), were deduced from clones (AAT45042-43) obtd. by PCR amplification. Isolation of the gene sequences allows the mass prodn. of recombinant CP2 in transformed host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori and in the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "residue 449 is Gly in CP2-PCR1 and CP2-PCR2 and
                                                                 note= "residue 130 is Asp in CP2-PCR2"
                                                                                           'note= "residue 160 is Pro in CP2-PCR2"
                                                                                                                      note= "residue 218 is Leu in CP2-PCR2"
                                                                                                                                               note= "residue 234 is Ile in CP2-PCR2"
                                                                                                                                                                                                     'note= "residue 248 is Asp in CP2-PCR2"
                                                                                                                                                                                                                                'note= "residue 262 is Ile in CP2-PCR2"
                                                                                                                                                                                                                                                        note= "residue 285 is Cys in CP2-PCR2"
                                                                                                                                                                                                                                                                                   'note= "residue 287 is Lys in CP2-PCR2"
                                                                                                                                                                                                                                                                                                             'note= "residue 292 is Thr in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                        'note= "residue 316 is Thr in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                   'note- "residue 344 is Cys in CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                              /note= "residue 358 is Arg in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "residue 397 is Thr in CP2-PCR2"
                                                                                                                                                                         note= "residue 237 is His
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            Helicobacter pylori strain ATCC 43504
                               Location/Qualifiers
130
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95JP-0136564.
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N-PSDB; AAT45041.
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Query Match Best Local Similarity

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Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori and in the production of vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "residue 160 is Pro in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "residue 234 is Ile in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CP2-PCR2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "residue 237 is His
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "residue 344 is Arg
and CP2"
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1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
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                         AAW06482 standard; Protein; 505 AA
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Pred. No. 1.7e-15;
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Tanaka T;

Sugiyama T,

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Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori and in
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                                                                                                                                                                                                                                             Claim 1; Page 21-23; 29pp; English.
                                                                                                      (WAKP ) WAKO PURE CHEM IND LTD
                                                               96JP-0083512.
                                         96EP-0108637
                                                                                                                                                                                                                     the production of vaccines
                                                                                                                               Kawabata T,
                                                                                                                                                       WPI; 1997-013697/02
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                                         30-MAY-1996;
                                                                                                                               Hirayasu K,
                                                                             02-JUN-1995;
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01-APR-1997;
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                                             in the specific and quantitative detection of H. pylori and in vaccine prodn. CP2 antibody titre shows high correlation with the pathology of gastritis. The CP2-PCR1 amino acid sequence was deduced from a DNA clone (AAT45042) obtd. by PCR amplification. Slightly different sequences were deduced for CP2 (AAW06481) from genomic DNA (AAT45041) and for CP2-PCR2 (AAW06483) from a PCR fragment (AAT45041) derived from a clinical isolate. Isolation of the gene sequences allows the mass prodn. of recombinant CP2 in transformed
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "residue 130 is Asn in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "residue 160 is His in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "residue 234 is Val in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "residue 248 is Asn in CP2 and CP2-PCR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in CP2 and CP2-PCR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "residue 287 is Gln in CP2 and CP2-PCR1"
                                     ATCC 43504 CP2-PCR1 antigen (AAW06482) is
                                                                                                                                                                                                                 Length 505;
                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "residue 449 is Arg in CP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "residue 262 is Val in CP2
                                                                                                                                                                                                         100.0%; Score 157; DB 18;
100.0%; Pred. No. 1.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; diagnosis; gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "residue 218 is His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "residue 237 is Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "residue 316 is Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "residue 292 is Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "residue 344 is Cys
                                                                                                                                                                                                                                                                  1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                              Claim 1; Page 18-20; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        AAW06483 standard; Protein; 505
                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter CP2-PCR2 antigen
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Best Local Similarity 100.
Matches 29; Conservative
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                                     Helicobacter pylori
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                                                                                                                                                   host cells.
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 Length 505;
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                                     Indels
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100.0%; Score 157; DB 18;
100.0%; Pred. No. 1.7e-15;
ive 0; Mismatches 0;
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                                                                                            1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                 AAW98423 standard; Protein; 505 AA
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97US-0833457.
97US-0881227.
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                                                                                                                                                                                                                                                                                                           H. pylori GHPO 358 protein
                                                                                                                                                                                                                                                                       (first entry)
                  Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                               peptic ulcer disease.
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The Helicobacter pylori catalase is a protein of 58650 Da. The protein, gene sequence and products, such as an immunogenic fragment, can be used for the treatment or prevention of Helicobacter infection, particularly H. pylori infections which cause gastroducdenal disease. They can also be used for the detection and diagnosis of Helicobacter infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Helicobacter catalase nucleic acid - used to develop products for the treatment or prevention of Helicobacter infection, particularly H. pylori gastroduodenal disease
                 Length 505;
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              Score 157; DB 19;
Pred. No. 1.7e-15;
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Pred. No. 7.1e-15;
 100.0%; Scor.
100.0%; Pred. No. 1.,...
... 0; Mismatches
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                                                                                                                                                                                                                                                              Helicobacter pylori isolate RU1 catalase.
                                                                                        Disclosure; Page 33-34; 46pp; English.
                                                                       1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
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(UYNE-) UNIV NEW SOUTH WALES
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Best Local Similarity 96.6
Matches 28; Conservative
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                                                                                                                          This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Helicobacter pylori catalase is a protein of 58650 Da. The protein, gene sequence and products, such as an immunogenic fragment, can be used for the treatment or prevention of Helicobacter infection, particularly H. Pylori infections which cause gastroducdenal disease. They can also be used for the detection and diagnosis of Helicobacter infection.
                                                                                                                                                                                                                                                                                                                    Gaps
                                        New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Helicobacter catalase nucleic acid - used to develop products for the treatment or prevention of Helicobacter infection, particularly H. pylori gastroduodenal disease
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                                                                                                 Claim 8; Page 711-713; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 37-38; 46pp; English
                                                                                                                                                                                                                                                                                                                                              1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
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(UYNE-) UNIV NEW SOUTH WALES.
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                                                                                                                                                                                                               detection and diagnosis.
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WPI; 1998-542293/46.
N-PSDB; AAX14142.
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Best Local Similarity
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Arabidopsis thaliana protein fragment SEQ ID NO: 27277.

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   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                             990S - 0.121825 .
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                                               Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG23826 standard; Protein; 394 AA
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61.9%;
990S-0151438.
990S-0151930.
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990S-0153076.
990S-0154018.
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990S-0159293.
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990S-01593295.
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990S-0159584.
990S-0160741.
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99US-0161359.
99US-0161360.
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99US-0161993.
99US-0162142.
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99US-0161405
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99US-0161920
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Best Local Similarity 61.99
watches 13; Conservative
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09-AUG-1
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Strong light adapting condition; light-resistant plant; transgenic plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY18131 standard; Protein; 492 AA.
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990S-0154779-
990S-0155486-
990S-0155659-
990S-0155659-
990S-0155659-
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990S-01571175-
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Matches 13; Conservative
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        22 - SEP - 1999;
24 - SEP - 1999;
26 - SEP - 1999;
26 - SEP - 1999;
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06 - OCT - 1999;
07 - OCT - 1999;
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21-OCT-1999;
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16-JUL-1999;
19-JUL-1999;
19-JUL-1999;
   This sequence represents a clone of the protein of the invention.

The invention relates to a gene that is induced and expressed in a plant under a strong light adapting conditions, and is prepared by a procedure of the following light inradiations (1) to (3) is made on a plant already irradiated by a light of a light intensity of 60-100 mu compared in the cell of said plant: (1) A light of a wave length component of a wave length component of a wave length of 300-700 mu E/sq. m s consisting of a continuous wave length component of a wave length region of 300-800 mm at 15-38 degrees C for a light of a light of a light intensity of 200-600 mu component of a wave length region of 350-500 mm at 15-38 degrees C for a long the region of 350-500 mm at 15-38 degrees C for several hours to several days; (2) a light of a light of an intensity of 200-600 mu component of a wave length region of 350-500 mm at 15-38 degrees C for several hours to several days; of a continuous wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length region of 300-800 mm component of a wave length 
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                                                           Induction of gene to be expressed in plant under a strong light adapting condition – useful for enabling plant to grow in desert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 53875.
                                                                                                        Claim 7; Page 12-13; 16pp; Japanese
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99US-0126264.
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99US-0127462.
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99US-0130077.
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99US-0123548
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Best Local Similarity 61.9%
Matches 13; Conservative
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            WPI; 1999-364702/31.
N-PSDB; AAX77100.
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99US-0142977.

99US-0143624 99US-0144005 99US-0144085. 99US-0144325 99US-0144331

99US-0144334 99US-0144335 99US-0144333

99US-0142920

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                                                                                                                                                                                                                Score 75; DB 21; Length 492;
Pred. No. 0.0054;
4; Mismatches 4; Indels
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ttnsgapvwnnnssmtvgprg 38
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61.9%;
        990S - 0159637
99US - 0159638
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                                                                                                                                                                                                                                  13; Conservative
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Best Local Similarity
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16-APR-1999;
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21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated catalase gene derived from Bacillus thermoglucosdasius useful for decomposing hydrogen peroxide in residual disinfectant remaining on
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                    Catalase; genetic engineering; hydrogen peroxide decomposition; contact lens; disinfectant.
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                                                                                                                                                           Length 512;
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                                                                                                                                                          Score 75; DB 21;
Pred. No. 0.0056;
                                                                                                                                                                             4; Mismatches
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990S-0160989.
990S-0161404.
990S-0161405.
990S-0161359.
       99US-0160814.
99US-0160815.
99US-0160980.
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97CN-0120386.
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99US-0161920.
99US-0161992.
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99US-0162142
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Best Local Similarity 61.9
Matches 13; Conservative
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                                   Gaps
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 DB 21; Length 483;
                                 5; Indels
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Score 71;
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                                   14; Conservative
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| 905-0137724 905-0138094 905-0138640 905-0138847 905-0139453 905-0139454 905-0139455 905-0139455 905-0139455 905-0139455 | 905. 0139462 905. 0139463 905. 0139463 905. 0139463 905. 0139817 905. 0140823 905. 0140823 905. 0141842 905. 0142803 905. 0142803 905. 0142803 905. 0142803 905. 0144085 905. 0144085 905. 0144085 905. 0144085 905. 0144085 | 990S-0144334. 990S-0144334. 990S-0144335. 990S-0144832. 990S-0144884. 990S-0144884. 990S-0145086. 990S-0145087. 990S-0145192. 990S-0145192. 990S-0145193. 990S-0145193. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145918. 990S-0145919. 990S-0147904. 990S-0147303. |
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PR 06-AnG-1999; 99US-0147416.

PR 10-AuG-1999; 99US-0147433.

PR 11-AuG-1999; 99US-0147433.

PR 11-AuG-1999; 99US-0147431.

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PR 11-AuG-1999; 99US-01481856.

PR 12-AuG-1999; 99US-014426.

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PR 21-AuG-1999; 99US-0149378.

PR 22-AuG-1999; 99US-0149329.

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PR 23

Query Match 44.6%; Score 70; DB 21; Length 115; Best Local Similarity 57.1%; Pred. No. 0.006; Matches 12; Conservative 4; Mismatches 5; Indels

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23-JUL-1999;
    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 33331.
                                                                                                                     AAG28201 standard; Protein; 492 AA
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ttnsgapvwnnnsaltvggrg 38
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                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Matches 12; Conserv
   13-AUG-1999;
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31-AU
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Query Match

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RR 22-JUN-1999; 990x-013895.

RR 22-JUN-1999; 990x-0140825.

RR 22-JUN-1999; 990x-0140827.

RR 02-JUL-1999; 990x-014326.

RR 12-JUL-1999; 990x-014332.

RR 13-JUL-1999; 990x-014433.

RR 13-JUL-1999; 990x-014432.

RR 13-JUL-1999; 990x-014433.

RR 13-JUL-1999; 990x-014433.

RR 22-JUL-1999; 990x-014538.

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for carifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The resent sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #3121 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 13415; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 57;
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Pred. No. 0.011;
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                                                                                                                                                       Rank DR;
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                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
2000US-0608408.
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66.7%;
30-JUN-2000; 2000US-060B40B.
03-AUG-2000; 2000US-063256.
21-SEP-2000; 2000US-02346B7.
27-SEP-2000; 2000US-0236359.
                                                                          04-OCT-2000; 2000GB-0024263.
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Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe of the invention.
                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                              WPI; 2001-496933/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW40229-W40247 are the N-terminal peptide fragments from various membrane proteins or membrane associated proteins isolated from Helicobacter pylori. Such N-terminal fragments could be used for therapeutic or diagnostic purposes, especially for developing vaccines against H. pylori infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #3098 encoded by breast cell single exon nucleic acid probe.
                                      Membrane protein; membrane associated protein; therapy; diagnostic;
vaccines; infection; adhesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori membrane proteins – useful for production of vaccines and antibodies for therapeutic and diagnostic purposes
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Pred. No. 0.0017;
); Mismatches 1; Indels

    H. pylori 63 kD adhesin N-terminal fragment.

                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                          'label- unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt K;
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92.98;
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26-MAY-2000; 2000US-0207456.
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                               Helicobacter pylori
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                                                                                                                                                                                            Misc-difference 10
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The present invention provides a number of single exon nucleic acid
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Matches 14; Conserv
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                          Sequence
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                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein #3043 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                       Claim 27; SEQ ID NO 28250; 639pp + sequence listing; English.
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cardiovascular disease; hypertension; cardiac arrhythmia;
congenital heart disease.
                                                                                                                                                                                                                                                                                        22; Length 57;
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Pred. No. (
                                                                   Chen W, Rank DR;
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                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                              ABB21044 standard; Protein; 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                            9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                        || | || | || || || || || || || || ttgagnpvgdklnvitvgprg 26
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03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                       42.0%;
66.7%;
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                           Conservative
                                                                   Hanzel DK,
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                                                                                       WPI; 2001-483447/52
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conserv
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
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                                                                                                                                                                                                                                                           Sequence
                                                                    SG,
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measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                                                                                                                 By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 28537.
exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human brains - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                          present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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Pred. No. 0.011;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                          Claim 15; SEQ ID No 22814; 530pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.0%;
66.7%;
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2000US-0207456.
2000US-0608408.
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2000US-0234687
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Peptide #3065 encoded by probe for measuring cervical gene expression

(first entry)

12-OCT-2001

AAM16631;

A.

AAM16631 standard; Protein;

53 26

TTAFGAPVWDDNNVITAGPRG

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Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer

Homo sapiens

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimmer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       Human bone marrow expressed probe encoded protein SEQ ID NO: 29119
                                                                                                                                                                                                                                                                                         bone marrow expressed exon; gene expression analysis; probe;
ray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                   57;
                                                                                                                       7; Indels
                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing gene expression in human bone marrow
                                                                                                   DB 22;
0.011;
                                                                                                                       Mismatches
                                                                                                   Score 66;
Pred. No.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234359.
                                                                                                   42.0%;
66.7%;
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                                                                                                                                                      (first entry)
                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53.
                                                                                                  Query Match
Best Local Similarity
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                    microarray;
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                                                                        Sequence
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                                                                                                                                                                                                                                                                                          Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer. Once: The square did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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analyzing gene expression in human cervical epithelial cells
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Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                 Rank DR;
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                                                                                                                                                                                                                                                                                                                 Chen W,
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                                                                           2001WO-US00670
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2000US-0608408
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                 Hanzel DK,
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Best Local Similarity
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WO200157278-A2
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26-MAY-2000;
30-JUN-2000;
                                                                           30-JAN-2001;
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                                    09-AUG-2001
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Gaps

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Indels

7;

0.011;

Score 66; DB Pred. No. 0.01 0; Mismatches

42.0%; 66.7%;

Best_Local Similarity 66.7 Matches 14; Conservative

Query Match

DB 22; Length 57;

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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                         Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Catalase; PCR; primer; amplification; expression; E.coli; decomposition; hydrogen peroxide; disinfectant; contact lens.
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Pred. No. 0.011
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID No 13088; 322pp; English.
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                                                                                                                                                                                                                                  Rank
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                                                                   2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                29-JAN-2001; 2001WO-US00661.
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                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
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                                                                                                                                                                                                                                                                                                                            in a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AA;
                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                      30-JUN-2000;
03-AUG-2000;
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                                                    04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                   Peptide #3154 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #3030 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                      microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66; DB :
Pred. No. 0.01:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID No 29386; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM04348 standard; Protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || | || | || || || || || || || || 6 ttgagnpvgdklnvitvgprg 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                        2000US-0207456.
2000US-0608408.
2000US-052366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.0%;
66.7%;
                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AA;
                                                                                                                         genetic disorder
                                                                                                                                                                                              WO200157272-A2.
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                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                             Homo sapiens,
                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                       04-FEB-2000;
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                                 17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-0CT-2001
                                                                                                                                                                                                                                09-AUG-2001
AAM29117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                      Probe:
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polynucleotide which comprises the sequence (1) given in the specification. The invention also describes 1) a catalase polypeptide comprising at least residues 127 to 509 of the fully defined amino acid given in the specification, 2) a recombinant vector carrying comprising the gene; and 3) a transformant transformed by the above recombinant vector. The catalase is useful as an enzymatic agent decomposing hydrogen peroxide contained in waste water.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Vibrio rumoiensis S-1 catalase polypeptide and polynucleotide for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel Vibrio rumoiensis S-1 catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Length 509;
                                                                                       Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Catalase; hydrogen peroxide decomposition; waste water.
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9
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                                                                                       DB 21;
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Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                        V. rumoiensis S-1 catalase protein SEQ ID 2.
                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                       Score 66;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
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                                                                                                                                                                                                                                                                                              AAB46776 standard; Protein; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP82004 standard; protein; 527
                                                                                                                                                              7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                 27
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                                                                                                                                                                                                 5 klttswgapvgdnqnsitagnpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.0%;
ilarity 61.9%;
Conservative
                                                                                     Query Match
Best Local Similarity 60.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0134831
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|4 ttdfgapvvtnrdsltagprg
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating waste water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-106416/12.
N-PSDB; AAF25916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio rumoiensis.
                                  483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2000316584-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1999;
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                                  Sequence
                                                                                                                                                                                                                                                                                                                                    AAB46776;
   enzyme.
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                                                                                                                                                                                                                                                                              AAB46776
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                                                                                                                                                                                                                                                                                                                                   XXXX
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SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a catalase isolated from Bacillus thermoglucosidasius. A composition containing a B. thermoglucosidasius catalase is used to decompose hydrogen peroxide present in residual disinfectant remaining on a contact lens to avoid undesired injury to users. The catalase enzyme can also be used to treat textile substances which have been bleached with hydrogen peroxide. The catalase is derived from a non-mammalian source and reducing the need to use boyine liver catalases so the risk of cross infection from cows to humans is reduced. The production procedure is simple and has low cost with high yield of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated catalase gene derived from Bacillus thermoglucosdasius useful for decomposing hydrogen peroxide in residual disinfectant remaining on
                                                                                                                                           This sequence corresponds to the catalase protein (kat 19) from the microorganism Bacillus thermoglucosidasius. The gene was PCR amplified and inserted into the plasmid pET-20b for expression in an organism such as E.coli DH5alpha. The protein can be used for the decomposition of hydrogen peroxide contained in the residual disinfectant remaining in a contact lens solution.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                    Preparation of catalase - useful for production of catalase in high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalase; genetic engineering; hydrogen peroxide decomposition; contact lens; disinfectant.
                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                   Score 66; DB 20; Length 483;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus thermoglucosidasius catalase kat TG SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                         ;
6
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78357 standard; Protein; 483 AA.
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                                                                                                          Page 3; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                           5 klttswgapvgdnqnsitagnpg 27
                                                                                                                                                                                                                                                                                                                                                                                                          7 KOTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOT-) DEV CENT BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                   42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thermoglucosidasius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97TW-0100018.
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                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
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N-PSDB; AAZ88397.
WPI; 1999-603710/52
                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                              483 AA;
                 N-PSDB; AAZ28794
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11-DEC-1997;
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                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                          Claim 3;
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                                                                       yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 28
                                                                                                                                                                                                                                                                                                                                                                       Matches
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Gaps

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Length 527; 7; Indels

DB 19;

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endometrium during the hyperplassa, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protection of mammalian cells against immunotoxicity or lipotoxicity - used for treating, e.g. diabetes, obesity, wasting syndromes, osteoporosis, inflammatory diseases, autoimmune diseases or neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell; fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis; inflammatory disease; autoimmune disease; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibition of cytokine mediated immunotoxicity of cells can be achieved by blocking free radical production or the accumulation of free radicals in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can be achieved by blocking nitric oxide (NO) production in a pancreatic beta cell and by providing a composition comprising an agent that reduces levels of fatty acids in the cells
                                                                                                      Proteins AAW54349-W54364 are examples of proteins produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manganese containing superoxide dismutase; MnSOD; IDDM;
  Biochemical markers of human endometrium - useful for,
                                                                                                                                                                                                                                                                                                                                 Score 66; DB 19
Pred. No. 0.14;
0; Mismatches
                   diagnosis of hyperplasia and adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 242-244; 253pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koyama K, Le
                                                               77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW96321 standard; Protein; 527 AA
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                                                                                                                                                                                                                                                                                                                                   42.0%;
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97US-0055092
                                                                                                                                                                                                                                                                                                                                                                                                                    9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hohmeier H, K
Shimabukurom,
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human catalase sequence.
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N-PSDB; AAX08433.
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                       527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9906059-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-1998;
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Ohneda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96321;
                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The DNA encoding the gene can be used to produce recombinant catalase which, with superoxide dismutase, is an important anti-
inflammatory factor in vivo and can be used as a drug.
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0
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2D gel electrophoresis; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       used to produce catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                Catalase; inflammation; antiinflammatory drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.14; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.0%; Score 66;
66.7%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1; 5pp; Japanese.
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96GB-0018600
                                                                                                                                                                                                                                                                                                                                                                                                                                                         for antiinflammatory drugs.
15-OCT-1990 (first entry)
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                                         Recombinant catalase
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N-PSDB; AAN82012.
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Matches 14; Conserv
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                                                                                                                                                                JP63017693-A.
                                                                                                                         Homo sapiens
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Lee Y, New A, Unger RH

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production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                      Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAW80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chmokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                   22; Length 527;
                                                                                                                                                                                                                                                                                                                   7; Indels
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u C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                 Score 66; DB 2
Pred. No. 0.14;
0; Mismatches
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Liu C, Wehrman T, Xu
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66.7%;
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-06631936.
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N-PSDB; AAI59024.
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Matches 14; Conserv
                                                                                                                                                                                                                             527 AA;
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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09-JUL-2000;
19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; socihe; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                          death. Cells can also be protected against nitric oxide mediated cytotoxicity by introducing into the cell an antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e. g. 1L-1 beta, 1L-1 alpha, gamma IFN, TNF alpha, TNF beta, 1L-8, IL-7, IL-7, IL-7, IL-7, IL-19, IL-14, IL-17, granulocyte-macrophage colony stimulating factor or monocyte chemoattractant protein-1. The methods can be used for the treatment of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting syndromes, short stature, osteoporosis, inflammatory diseases, autoimmune diseases, or neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                     Gaps
             protects beta-cells of the subject against lipid-mediated cell
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66.7%; Pred. No. 0.14;
ive 0; Mismatches 7; Indels
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R, Ψέ
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Wang D, Wang J, Zh
Yang Y, Wejhrman T,
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2000US-0560875.
2000US-05208075.
2000US-0620325.
2000US-0654936.
2000US-0653351.
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Best Local Similarity
Matches 14; Conserv
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20-JUN-2000;
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20-OCT-2000;
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Zhao QA,
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Zhang J;

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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, archititis and inflammation, leukaemias and
                                                                                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                      peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hantington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Darger Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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19-JUL-2000; 2000US-0620312.
03-AMG-2000; 2000US-0633450.
14-SRP-2000; 2000US-0653036.
19-OCT-2000; 2000US-0693036.
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Best Local Similarity 66.7°
Matches 14; Conservative
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N-PSDB; AAI60810.
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                                                                                                                                                specification
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The invention relates to human nucleic acids (AAL57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemctactic/chemckinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Κ;
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Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66; DB 22
Pred. No. 0.15;
0; Mismatches
Example 2; SEQ ID NO 6585; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM79424 standard; Protein; 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein SEQ ID NO 3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20000S-0560875.
20000S-0598075.
20000S-0620325.
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20000S-0663561.
20000S-0693325.
2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.0%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                           C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            558
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20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                             specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36
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                                                                                                         encoded polypeptides (AAM/8032) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                Note: Measurements.

Note: Records for SEO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a wheat catalase gene which is inserted in a rice genome in order to improve cold-resistance. Such a cold-resistant catalase is useful for the decomposition of hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                               The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene - useful for producing
the decomposition of hydrogen
Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catalase; rice; wheat; plant; cold-resistance; hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 66; DB 22; Length 565; Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK.
                                                         6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice having cold-resistance catalase cold-resistant rice and catalase for peroxide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOKU-) HOKUREN NOGYO KYODO KUMIAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 12; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW63845 standard; Protein; 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                       Claim 20; Page 242-243;
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              565 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          decomposition.
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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The present sequence is a rat mitogenic oxidase mox1B
which is capable of stimulating production of superoxide, a reactive
oxygen intermediate (ROI) that affects cell division. The present
sequence was obtained from a rat convalidation. The present
sequence was obtained from a rat convalidation. The present
cells exposed to angiotensin II. Mox1B is a spliced variant of rat mox1,
also referred as p65mox. The mox1B protein functions as a mitogenic
regulator. The present sequence is useful in developing
regulator. The present sequence is useful in developing
frowth, including cancer, psoriasis, prostatic hypertrophy, benign
prostatic hypertrophy, cardiovascular disease, proliferation of vessels,
c e.g. blood vessels and lymphatic vessels, arteriovenous malformation,
vascular problems associated with eye, atherosclerosis, hypertension,
and restenosis following angioplasty.
                                 ö
                                                                                                                                                                                                                                                                                                                 Rat; mitogenic regulator; mox1B; mitogenic oxidase; p65mox; superoxide; reactive oxygen intermediate; RoI; cell division: cytostatic; antipsoriatic; cardiant; antiarteriosclerotic; vasotropic; antiangiogenic; hypotensive; drug development; treatment; cancer; abnormal growth; psoriasis; prostatic hypertrophy; proliferation; blood vessel, 'Imphatic vessel; benign prostatic hypertrophy; cardiovascular disease arteriovenous malformation; eye disorder; hypertension; atherosclerosis; restenosis; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein capable of stimulating superoxide production, useful for treating conditions associated with abnormal growth, including cancer
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guangjie C;
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Score 64; DB 19; Length 492;
Pred. No. 0.26;
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                                 5;
                                   Mismatches
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                                                                                                                                                                                     AAY71122 standard; Protein; 499 AA.
                                                                                                                                                                                                                                                                                        Rat mitogenic regulator mox1B.
                                                                   53
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99US-0149332.
99US-0151242.
 40.8%;
52.4%;
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                                                                                        9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                       (first entry)
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                 Best Local Similarity 52.4
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1999;
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27-AUG-1999;
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                                                                                                                                                                                                                                                       08-SEP-2000
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   Query Match
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Length 499;

DB 21;

38.9%; Score 61;

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Sequence

Query Match

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Gaps

5

Indels

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Mismatches

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6 VKQTTAFGAPVWDD--NNVITAGPR
      11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           treatment
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        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   also referred as p65mox, which is capable of stimulating production of superoxide, a reactive oxygen intermediate (ROI) that affects cell superoxide, a reactive oxygen intermediate (ROI) that affects cell superoxide, a reactive oxygen intermediate (ROI) that affects cell smooth muscle cell. The mox1 protein functions as a mitogenic regulator and shows homology to human mox1 protein. It is expressed in aortic and shows homology to human mox1 protein. It is expressed in aortic smooth muscle cells and induced by angiotensin II, platelet-derived growth factor (PDGF) and phorbol myristic acid (PMA).

The present sequence is useful in developing qrough and therapies for treatment of conditions associated with abnormal growth, including cancer, psoriasis, prostatic hypertrophy, cardiovascular disease, proliferation of vessels and lymphatic vessels, arteriovenous malformation, wascular problems associated with eye, atherosclerosis, hypertension,
                                                                                                                                                                                                                                                                                                                                                                   Rat; mitogenic regulator; mox1; mitogenic oxidase; p65mox; superoxide; reactive oxygen intermediate; ROI; cell division; cytostatic; antipsoriatic; cantidant; antiarteriosclerotic; vasotropic; antiangiogenic; hypotensive; drug development; treatment; cancer; abnormal growth; psoriasis; prostatic hypertrophy; proliferation; blood vessel; lymphattc vessel; benign prostatic hypertrophy; cardiovascular disease; arteriovenous malformation; eye disorder; hypertension; atherosclerosis; restenosis; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein capable of stimulating superoxide production, useful for treating conditions associated with abnormal growth, including cancer
                           Gaps
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                         5
                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a rat mitogenic oxidase mox1,
                         5,
  44.0%; Pred. No. 0.75;
tive 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 98-100; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and restenosis following angioplasty
                                                                                       :|| |:|| |:||: | : || |:
434 lkqktsfgrpmwdnefsriatahpk 458
                                                              6 VKQTTAFGAPVWDD--NNVITAGPR 28
                                                                                                                                                                                                        AAY71121 standard; Protein; 563
                                                                                                                                                                                                                                                                                                                               Rat mitogenic regulator mox1.
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                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 44.0
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                       08-SEP-2000
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27-AUG-1999;
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Score 61; DB 21; Length 563; Pred. No. 0.86;

38.9%; 44.0%;

Query Match Best Lącal Şimilarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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45.0%; Pred. No. 0.55;
iive 5; Mismatches 6
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498 lkqktsfgrpmwdnefsriatahpk
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Matches 9; Conserv
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Run

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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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-08-704-711A-22
-08-448-489-11
-08-464-052-2
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                                                                                                                                                                                                             hits satisfying chosen parameters:
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-09-027-166-9

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-09-126-109-10
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Maximum Match 100%
Listing first 100 summaries
                                                  - protein search, using sw model
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seq length: 200000000
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Match
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Maximum DB :
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Sequence 14, Appl Sequence 15, Appl Sequence 17, Appl Sequence 18, Appl Sequence 21, Appl Sequence 22, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 25, Appl Sequence 26, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 33, Appl Sequence 34, Appl Sequence 34, Appli Sequence 54, Appli

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Sequence Sequence Sequence Sequence

Sequence 2 Sequence 2 Sequence 2

Sequence

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Sequence Seq

App1;

Sequence

Sequence 47, Sequence 6,

STREET: 130 Water Street

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Query Match 100.0%; Score 157; DB 3; Length 505; Best Local Similarity 100.0%; Pred. No. 5.4e-17; Matches 29; Conservative 0; Mismatches 0; Indels (
                                                                            COMPUTER REACABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OURRAIT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NAMBER: US/08/657,868B
FILING DATE: 31-MAY-1996
CLASSIFICATION TATA:
APPLICATION NUMBER: 136465
FILING APPLICATION DATA:
APPLICATION NUMBER: 136465
FILING DATE: 03-JON-1995
APPLICATION NUMBER: 83512
FILING DATE: 05-MR-1995
APPLICATION NUMBER: 83512
FILING DATE: 05-JON-1995
APPLICATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 34,235
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TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acids
STRANDEDNESS: single
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                                         USA
Boston
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US-08-657-868B-5
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                                         COUNTRY:
                  STATE:
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                                                                                                                                                                                                             APPLICANT: ACIDED, ALLISTOPHEL V.
APPLICANT: RADGLIFF, Fiona J.
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES:
ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 505;
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Patent No. 6080556
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STGITAMA, TOMOLISA
APPLICANT: HIRXASU, KAZUNATI
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCES:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,987
FILING DATE: 15-AUG-1996
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Best Local Similarity 100.0%; Pred. No. 5.4
Matches 29; Conservative 0; Mismatches
                    ALIGNMENTS
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                                                                                                                                                                                        DOIDGE, Christopher V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17227
TELECOMMUNICATION INFORMATION:
TELEFEAX: (202)672-5300
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
                                                                                                                         Sequence 4, Application US/08695987
Patent No. 6005090
GENERAL INFORMATION:
APPLICANT: DOIDGE, Christopher V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-695-987-4
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US-08-657-868B-4
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APPLICANT: KAWABRTA, TOMONISA
APPLICANT: HIRATASU, KAZUNATI
APPLICANT: HIRATASU, KAZUNATI
APPLICANT: HIRATASU, TAZUNATI
APPLICANT: FRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SECUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIAN
SYSTEM: DOS
SOFTWARE: FastESG for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/657,868B
                                                     1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                   1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                  Sequence 5, Application US/08657868B Patent No. 6080556 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: DEE, Adrian
APPLICANT: RADCLIFF, Fiona J.
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
TORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STRRET: 3000 K Street, N.W., Suite 500
CITY: Washington
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                                                                                                                                                                                                                                                                                         Length 505;
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ZIP: 20007-5109

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/695,987

FILING DATE: IB-AUG-1996

CLASSIFICATION: 18-AUG-1996

ATONIRY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 153; DB 3; L
Pred. No. 2.4e-16;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 157; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.4e-17;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-008-695-987-2
; Sequence 2, Application US/08695987
; Patent No. 6005090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202)672-5300
TELERAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
                              TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.5%;
Best Local Similarity 96.6%;
Matches 28; Conservative
617-523-3400
                   TELEFAX: 617-523-6440
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-695-987-2
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                               US-08-657-868B-6
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CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: STGAINA, TOSILO
APPLICANT: KAMABATA, TOMONISA
APPLICANT: HIRAYASU, KAZUNATI
APPLICANT: HIRAYASU, KAZUNATI
APPLICANT: TANAKA, TAKUMI
TITLE OF INVEWTION: POLYPEPTIDES, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 157; DB 3; Best Local Similarity 100.0%; Pred. No. 5.4e-17; Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,868B
FILING DATE: 31.MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08657868B Patent No. 6080556
                                                                                                                                                           NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 4652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 136465
FILING DATE: 02-UN-1995
APPLICATION NUMBER: 83512
FILING DATE: 05-APR-1996
ATTORNEY/AGENT INFORMATION:
                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 136465
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: 83512
FILING DATE: 05-ARR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
FILING DATE: 31-MAY-1996
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-657-868B-6
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Gaps
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60.9%; Pred; No. 0.0027;
Virmatrhes 5; Indels
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
COMPOTER: TBM PC compatible
COMPOTER: DEAD PC COMPOTER:
COMPOTER: DEAD PC COMPOTER:
COMPOTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,166
FILING DATE: 20-FEB-1998
CRASSIFICATION NUMBER: TW 8610018
FILING DATE: 03-JAN-1997
PRIOR APPLICATION NUMBER: CN 97120386.5
FILING DATE: 11-DEC-1997
ATTORNEY/AGENT INDEX: 98,180
FELENGOMANICATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 98,180
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION OF 9:
SEQUIENCE CHARACTERISTICS:
SEQUIENCE CHARACTERISTICS:
SEQUIENCE CHARACTERISTICS:
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ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/027,166
FILING DATE: 20-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | ||::|||| |: | :||| || 5 KLTTSWGAPVGDNQNSMTAGSRG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I: 483 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-09-027-166-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
    Chicago
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                                         USA
                                                         ZIP: 60606
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                                         COUNTRY:
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| Sequence 9, Application US/09027166
| Sequence 9, Application US/09027166
| Sequence 9, Application US/09027166
| Patent No. 6022271
| GENERAL INFORMATION:
| APPLICANT: HWONG, Ching-Long
| APPLICANT: HWONG, Ching-Long
| TITLE OF INVENTION: Composition Comprising The Same, And Process For Preparing
| TITLE OF INVENTION: Catalase Using Genetic Engineering Technology
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MCDonnell Boehnen Hulbert & Berghoff
| STREET: 300 S. Wacker Drive Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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0
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APPLICANT: LEE, Adrian
APPLICANT: LEE, Adrian
APPLICANT: RADCLIFF, Flona J.
APPLICANT: RADCLIFF, Flona J.
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                ADDRESSE: Folgy & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,987
FILING DATE: 15-AUG-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73; DB 3;
Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
17227/128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 1722;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
                                                                                           %3-08-695-987-6
; Sequence 6, Application US/08695987
; Patent No. 6005090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVNKDVKQTTAFGTP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-08-695-987-6
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US-08-365-486A-26
Sequence 26, Application US/08365486A
Sequence 26, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                        42.0%; Score 66; DB 4; Length 527; 66.7%; Pred. No. 0.019; 1ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.3%; Score 57; DB 4; Length 495; 52.4%; Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCORATION:
APPLICANT: Chalfie, Martin
APPLICANT: Taub, James J.
TITLE OF INVENTION: A METHOD FOR INCREASING LIFE-SPAN
FILE REFERENCE: 0575/51778/JPW/JSG
CURRENT APPLICANTION NUMBER: US/08/980,241D
CURRENT FILING DATE: 1997-11-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/08980241D
; Patent No. 6319708
LELEPAX: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acids
STRANDEDNESS:
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                            9 TTAFGAPVWDDNNVITAGPRG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.3
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                          Query Match 42.0
Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                    TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-126-109-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Nematodes
US-08-980-241-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-980-241-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB 3;
Pred. No. 0.017;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-0UL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNKNOWN
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: MCMIllian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:560
                                                                                                                  NAME: CHAO, MARK
REGISTRATION NUMBER: 37,293
REPERENCE/CDCKET WUMBER: 98,180
TELECOMMUNICATION INFORMATION:
TELEFAKN: (312) 913-0001
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Thigpen, Anice
APPLICANT: Hohmeler, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Newgard, Christopher B.
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Rhodes, Christopher J.
APPLICANT: Cousin, Sharon
                                                          APPLICATION NUMBER: CN 97120386.5 FILING DATE: 11-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
APPLICATION NUMBER: TW 86100018 FILING DATE: 03-JAN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09126109
Patent No. 6171856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 KOTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.0%;
60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.95
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-027-166-7
                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Texas
COUNTRY: USA
ZIP: 77210
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                                                                                                                                                                                                                                      DB 4; Length 527;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-846-181-5

Sequence 5, Application US/07846181

Patent No. 5360732

GENERAL INFORMATION:

APPLICANT: BERKA, RANDY M

APPLICANT: FOWLER, TIMOTHY

APPLICANT: FOWLER, TIMOTHY

APPLICANT: FOWLER, TROTHY

TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER

TITLE OF INVENTION: CATALASE-R

NUMBER OF SEQUENCES: 9

CORRESPENDENCE ADDRESS:

ADDRESSE: GENENCOR INTERNATIONAL, INC.

STREET: 180 KIRBALL WAY

CITY: SOUTH SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/07/846,181
FILING DATE: 19920304
FLING DATE: 19920304
ATTORNEY/AGENT INFORMATION:
NAME: HORN MS, MARGARET A
REGISTRATION NUMBER: 33401
REFERENCE/DOCKET NUMBER: GC204-US1
TELEPHONINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                   35.7%; Score 56; 52.4%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/07845989; Patent No. 5360901; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                  28 TTGGNPIGDKLNIMTAGSRG 48
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   : 527 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 730 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || || || : | : |||||| 59 TIDFGTPI-SDQTSLKAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-742-7217
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.47
                                                                                                                                                                                                                                                                                                 Conservative
                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-342-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-07-846-181-5
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-07-845-989-5
      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/0880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Laderoute, Keith R.
APPLICANT: Laderoute, Keith R.
APPLICANT: Tries of INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE STATEM 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CURRELL
APPLICATION
FILING DATE: 23-DEC
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TVPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sholtz, Charles K.
REGISTRATION UNBABR: 38,615
REFERENCE, DOCKET UNBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Cambridge Avenue, Suit CITY: Palo Alto STATE: CA COUNTY: USA 2IP: 94306 COMPUTER READABLE FORM: MEDIUW TYPE: Floppy disk COMPOTER: IBM PC COMpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 TTGGGNPIGDKLNIMTAGSRG 48
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TELEFAX: (415) 334-0960
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.49
Watches 11; Conservative
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Sequence 2, Application US/09061768A

Patent No. 6204037

GENERAL INFORMATION:

APPLICANT: BRASH, ALAN R.

APPLICANT: BRASH, MITSUO

TITLE OF INVENTION: LIFOXYGENASE PROTEINS AND NUCLEIC ACIDS

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: ALTALES A. TAYLOR, JR.

STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

CITY: DURHAM

STREET: SOUTH CAROLINA

COUNTRY: USA

ZIP: 27707

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: WINDOWS 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

CLASSIFICATION NUMBER: US/09/061,768A

FILING DATE: APPLICATION DATA: NONE

APPLICATION DATA: NONE

APPLICATION DATA: NONE

APPLICATION DATA: NONE
                                                                                                                                                                                                                                                                                                                                                                                                                                      31.8%; Score 50; DB 1; Length 1188; 47.4%; Pred. No. 18; 7; Indels tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 676;
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Pred. No. 13;
                                                                                                                                                P-UM 9783
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryb A.
REGISTATION UNMBER: 31,815
REFERENCE/DOCKET UNMBER: P-UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.2%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KOTTAFGAPVWDDNNVITA 25
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SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 47.4 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-201-697-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Wiggins, Roger C.
APPLICANT: Thomas, Peedikayil E.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
APPLICANT: BERKA, RANDY M

APPLICANT: FOWLER, TIMOTHY

APPLICANT: REY, MICHAEL W

TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
TITLE OF INVENTION: CATALASE-R

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENTWATT
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/07/845,989
FILING DATE: 19920304
CLASSIFICATION NUMBER: US/07/845,989
FILING DATE: 19920304
CLASSIFICATION NUMBER: US/07/845,989
FILING DATE: 19250304
CLASSIFICATION NUMBER: US/07/845,989
FERENCE/DATION NUMBER: US/07/845,989
FERENCE/DATION NUMBER: GC208-US1
REFERENCE/DOCKET NUMBER: GC208-US1
TELEPHONE: 415-742-721
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: ANINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...wresSE: ...wresS:
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: Callfornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,697
FILING DATE: 25-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52.5; DB Pred. No. 4; 2; Mismatches
                                                                                                                                                                                                                                  ADDRESSEE: GENENCOR INTERNATIONAL, INC. STREET: 180 KIMBALL WAY CITY: SOUTH SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5705623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.4%;
Best Local Similarity 52.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-07-845-989-5
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                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                          COUNTRY:
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US-08-201-697-4
                                                                                                                                                                                                                                                                                CITY: STATE:
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GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Pele
TITLE OF INVENTION: DIA MOLECULE FRAGMENTS ENCOBING FOR
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Navon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.3%; Score 44.5; DB 3;
33.3%; Pred. No. 23;
tive 6; Mismatches 9;
                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/327001
TELECOMMULCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/185,370
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                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/08689411; Patent No. 6224881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISICS:
LENGTH: 271 amino acids
TYPE: amino acid
                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-185-370-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 536
                                                                                       STATE: MA
COUNTRY: US
TP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York COUNTRY: U.S.A.
                                                                                 Boston
                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-689-411-8
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  8; Indels
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                                                                                                                                                                       Sequence 4, Application US/08852743;
Patent No. 5830699;
GENERAL INFORMATION:
APPLICANT: Force, Thomas
APPLICANT: Force, John M.
APPLICANT: Force, Joseph;
TITLE OF INVENTION: SOR-1 AND METHODS OF USE;
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,743
FILING DATE: 7-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/016,774
FILING DATE: 7-MAY-1996
ATORNEY/AGENT INFORMATION:
NAME: Fraser. 7-MAY-1996
ATORNEY/AGENT INFORMATION:
NAME: Fraser. 30 and 8 / REGISTRATION NUMBER: 34,819
REFERENCE/ODCKET NUMBER: 00786/327001
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Force, Thomas
APPLICANT: Kyriakis, John M.
APPLICANT: Rombo, Celia M.
APPLICANT: Bonventre, Joseph
TITLE OF INVENTION: SOK-1 AND METHODS OF USE
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|:|| | | | |:: ||:
153 NIKRTTMVGTPYWMAPEVVSRKEYGPK 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09185370 Patent No. 6093560 GENERAL INFORMATION:
  ;
                                      11 AFGAPVWDDNNVITAGPRG 29
                                                               13 AFGAGTWDKVSVSIVGTRG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-852-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                       US-08-852-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-185-370-4
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                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
  Matches
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Sequence 4, Application US/08689411 Patent No. 6224881
                                                                                                       Sequence 4, Application US/08461002 Patent No. 6214543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.0
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
; FRAGMENT TYPE: unknown
US-08-461-002-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | |:| || ||
1 VNADIKATTVFG 12
2 VNKDVKQTTAFG 13
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                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                      US-08-461-002-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-689-411-4
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APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 20;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                            DB 4; Length 60;
                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                            Score 44; DB Pred. No. 4.5; 1; Mismatches
             NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/CDCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716, 263-1304
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08464052
Patent No. 6008201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.0%;
66.7%;
                                                                                                                                                                                                                                                                                                        Query Match 28.0%;
Best Local Similarity 66.7%;
Matches 8; Conservative
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 66.7.
انام 8. Conservative
                                                                                                                                                                  LENGTH: 60 amino acids TYPE: amino acid
                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
FRAGMENT TYPE: unknown
                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-689-411-8
                                                                                                                                                                                                                                                                                                                                                                                                      2 VNKDVKQTTAFG 13
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                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                      TOPOLOGY:
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2 VNKDVKQTTAFG 13

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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Uptake of Mycobacterium Tuberculosis and Uses thereof
INUMBER OF SEQUENCES:
Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES:
UNIXON, Hargrave, Devans & Doyle
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
IP: 14603
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002 GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF ö ; 0 Score 44; DB 4; Length 209; Pred. No. 20; 1; Mismatches 3; Indels NAME: Goldman, Michael L.

REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: U.S.A.

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US-08-01-71-2
Sequence 2, Application US/08001711
Sequence 2, Application US/08001711
Sequence 2, Application US/08001711
Sequence 3, Application US/08001711
Sequence 4, Application 548476
Sequence 5, Application 5, Applicant BASSET, PAUL
SEQUENCE 5, Application FIRE
TITLE OF INVENTION: ANALYTICAL MARKERS FOR MALIGNANT BREAST
TITLE OF INVENTION: CANCER
SUMBER OF SEQUENCES: ADDRESSE: ADDRESSE: Sterne, Gessler, Goldstein & Fox
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Pred. No. 57;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                      Score 44; DB 1; Length 488;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCES:
CORRESPONDENCESS:
CORRESPONDENCESS:
CORRESPONDENCESS:
STREET: 1225 Connecticut Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20056
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDAPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,711
FILING APPLICATION 435
PRIOR APPLICATION WHERE: US 07/794,393
FILING APPLICATION NUMBER: GB 9025626.1
FILING APPLICATION DATA:
APPLICATION NUMBER: GB 9025626.1
FILING APPLICATION DATA:
APPLICATION NUMBER: GB 9025626.1
FILING APPLICATION DATA:
APPLICATION NUMBER: GB 9025626.1
FILING DATE: LANOV-1990
ATTONENEY/AGENT INFORMATION:
ANDER ANDER THEORAMATION:
ANDER ANDER THEORAMATION:
ANDER ANDER THEORAMATION:
ANDER ANDER THEORAMATION:
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REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1383.0040001
                                                                                                                                                                                                                                                                                                                                                                                                                                          :| : |:|| | :|
121 LVQEQVRQTMAEALKVWSDVTPLT 144
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TELEPHONE: (202)466-0800
TELEFAX: (202)833-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.0%;
                                                                                                                                                                                                                                                                      28.0%;
37.5%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 488 amino acids
TYPE: AMINO ACID
                                             TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-794-393-2
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.55
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.5
                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-001-711-2
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Sequence 2, Application US/07794393
Sequence 2, Application US/07794393
Setuence 2, Application US/07794393
Setuence 2, Application US/07794393
Setuence 2, Application US/07794393
Setuence 2, Application US/07794393
APPLICANT: CHAMBON, PIERRE
APPLICANT: BELLOCQ, JEAN-PIERRE
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 4; Length 209;
Pred. No. 20;
1; Mismatches 3; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMan, Michael L.
REGISTRATION NUMBER: 30,727
REDERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,393
FILING DATE: 19911121
CLASSIFICATION NUMBER: GB 9025326.1
FILING DATE: 21-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAMME: GOLDSTEIN, JORGE A
REGISTRATION NUMBER: 29,021
REFERENCE/POCKET NUMBER: 1383.0040000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1225 Connecticut Ave. NW Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.0
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |:| || ||
1 VNADIKATTVFG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Gaps

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Sequence 2, Application US/08464052

Sequence 2, Application US/08464052

Patent No. 6008201

GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051

CITY: Rochester
STREET: U.S.A.
                                                                                                                                                                                                                  OTHER INFORMATION: Description of Unknown Organism: Known Member of OTHER INFORMATION: Matrix Metalloproteinase Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 60;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                               Score 44; DB 4; Length 489;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19603/185 (D-1485B)
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 14603
COMPUTER READABLE FORM:
CMBUUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LVQEQVRQTMAEALKVWSDVTPLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVNKDVKQTTAFGAPVWDDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
CURRENT FILING DATE: 1995-06-07
                                                                                                                                                                        OTHER INFORMATION: X = UNKNOWN
                                                                                                                                                                                                                                                                                                                               Query Match 28.0%;
Best Local Similarity 37.5%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.0%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 511 amino acids
amino acid
                    NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-464-052-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || |:| || ||
61 VNADIKATTVFG 72
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Best Local Similarity
8; Conserve
                                                                                                        TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                US-08-448-489-11
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Patent No. 6184022

GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SINAGAMA, Akira
APPLICANT: SINAGAMA, Akira
APPLICANT: SINAGAMA, Akira
FILLE REFERENCE: 55-290P

CURRENT APPLICATION NUMBER: US/08/448,489
                                                     Sequence 22, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, HOTST
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: MATALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Mashington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 1 LBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 21-OCT-1994
PRIOR APPLICATION NUMBER: DE 449863.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, PATICIA D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 33,683
TRELEPHANICATION INFORMATION:
TELEFERX: (202)672-5309
TELEFEXX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No
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121 LVQEQVRQTMAEALKVWSDVTPLT 144
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                                                                                                                                                                                                                                                                                                                                                             ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 488 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 28.0%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-704-711A-22
             RESULT 25
US-08-704-711A-22
                                                                                                                                                                                                                                                                                                                             STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-448-489-11
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Gaps

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28.0%; Score 44; DB 4; Length 511; 66.7%; Pred. No. 60;
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APPLICANT: Riley, Lee W.
APPLICANT: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%; Score 44; DB 5; Length 511;
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/689,411
FILING DATE:
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716,263-1000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: GOLDAm, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/187
RELECOMMUNICATION INFORMATION:
FELEPHONE: (716) 263-1304
TELEPHORE: (716) 263-1304
TELERAX: (716) 263-1304
TELERAX: (716) 263-1304
TELERAX: (716) 263-1304
TELERAX: (715) 263-1304
TELERAX: (715) 263-1304
TELERAX: (715) 263-1304
TYPE: amino acids
TYPE: sinilo acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 511 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-689-411-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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61 VNADIKATTVEG 72
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-09863-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US94-09863-2
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Sequence 2, Application US/08689411

Patent No. 62248H

GENERAL INFORMATION:

APPLICANT: Riley M.D., Lee W.

APPLICANT: Chong, Pele

TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CORRESPONDENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
, MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    Sequence 2, Application US/08461002 Patent No. 6214543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 511 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York COUNTRY: U.S.A. ZIP: 14603
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Best Local Similarity
Matches 8; Conserv
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CITY: Rochester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 14603
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                                   RESULT 28
US-08-461-002-2
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Pred. No. 88;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Broomlield, Clarence A
APPLICANT: Broomlield, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
CORRESPONDENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SISTEM: FC-LUCYMS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 32,535
TELEPRANICATION OF 25,2767
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
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Pred. No. 88;
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                                                                                                                                                                                                                                                                                                                                                                                                      2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08446100 Patent No. 6001625 GENERAL INFORMATION:
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50.0%;
                                                                                                                                                                                                                                                                                                             Query Match 27.7%;
Best Local Similarity 50.0%;
Matches 14; Conservative :
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                                                                                                                                                                                                                             ; ORGANISM: human esterases US-08-446-100-1
                                                                                                      MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGKENT TYPE: N-terminal
ORIGINAL SOURCE:
                  LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 602 amino acids
amino acid
    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                       Gaps
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Patent No. 6072048

GENERAL INFORMATION:
TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR UPTAKE OF
TITLE OF INVENTION: WYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
TITLE OF INVENTION: WYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
TITLE OF INVENTION: WYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/08/907,229A
CURRENT FILING DATE: 1997-08-06
EARLIER APPLICATION NUMBER: 60/040,097
EARLIER FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 527;
62;
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                       Indels
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION:
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REERRENCE/DOCKEY NUMBER: 32,535
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TO A25-4250
TELEPRAX: (703) 425-4250
                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Hendricks and Assoc.
9669 A Main Street, P.O. Box 2509
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  Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.0%; Score 44;
66.7%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-08-907-229-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.0
Best Local Similarity 66.7
Matches 8; Conservative
Best Local Similarity 66.7
Matches 8; Conservative
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179 VNADIKATTVFG 190
                                                                 2 VNKDVKQTTAFG 13
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STREET: 9669 A
CITY: Fairfax
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ZIP: 22031
                                                                                                                                                                               RESULT 31
US-08-907-229-2
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LENGTH: 527
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APPLICANT: Broamfield, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWN APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                         ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
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50.0%; Pred. No. 88;
ive 5; Mismatches
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CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL O
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                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
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                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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Best Local Similarity 50.0
Matches 14; Conservative
   NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: single
unknown
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STREET: 900.
TWY: Fairfax
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STATE: VA
COUNTRY: US
22031
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COUNTRY: US
ZIP: 22031
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      Gaps
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                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 602;
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Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.7%; Score 43.5; D
50.0%; Pred. No. 88;
tive 5; Mismatches
   5; Mismatches
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                                                                                               349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
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                                                            2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                       US-08-446-100-3; Sequence 3, Application US/08446100; Patent No. 6001625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION UNDRER: 32,535
REFRENCE/DOCKET UNDRER: broof
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 425-4250
IELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.09
Matches 14; Conservative
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESS: single
unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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Matches
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Gaps
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                                                                                                                                        Score 43.5; DB 3; Length 602;
Pred. No. 88;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Broomfield, Charles B
APPLICANT: Millard, Charles B
APPLICANT: LOCKINGS, OKSANA
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22031
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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                                                                                                                                                                                                                             2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                 US-08-446-100-7; Sequence 7, Application US/08446100; Patent No. 6001625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFRENCE/DOCKET NUMBER: broo
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 425-4250
TELEFRAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                            27.7%;
50.0%;
                                                             ORGANISM: human esterases US-08-446-100-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
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amino acid
                       N-terminal
                                                                                                                                            Query Match
Best Local Similarity 50.08
Matches 14; Conservative
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ANTI-SENSE: YES
FRAGMENT TYPE: N
ORIGINAL SOURCE:
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US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Broomfield, Clarence A
APPLICANT: Broomfield, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTE: Z2031

COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Hendricks Glenna
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43.5; DE Fred. No. 88; 5; Mismatches
                                                                                 broomfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
              ATTORREY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION UNDRER: 32,535
REFERENCE/DOCKET NUMBER: broom
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 maino acids
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        %3-08-446-100-6; Sequence 6, Application US/08446100; Patent No. 6001625; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.7%;
50.0%;
                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
AWTI-SENSE: YES
FRACMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.03
Matches 14; Conservative
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 22031
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DB 3; Length 602;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 32,535
RELECOMMUICATION INFORMATION:
TELEFAK: (703) 425-2767
THORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.7%; Score 43.5; D
Best Local Similarity 50.0%; Pred. No. 88;
Matches 14; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: YES
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ORIGINAL SOURCE:
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Sequence 11, Application US/08446100

Patent No. 6001625

GENERAL INFORMATION:

APPLICANT: Broomfield, Clarence A APPLICANT: Lockridge, Oksana

TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hendricks and Assoc.

STREET: 966 A Main Street, P.O. Box 2509

STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 602;
                                                                                 APPLICANT: Brondfeld, Clarence A
APPLICANT: Brondfeld, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                               ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CIIY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.7%; Score 43.5; Dest Local Similarity 50.0%; Pred. No. 88; Matches 14; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                          Sequence 8, Application US/08446100 Patent No. 6001625 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: human esterases US-08-446-100-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
          US-08-446-100-8
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|--|---|--|--|--------------------------------------|----------------------------------|---|------------------------------|--|---|--|--------------------|--|--|---|---------------------------------------|--|-------------------|--------------------|--------------------------------------|---|--|-------|---------------|---|--------------------------|
| 492 2 T06478 492 2 S52079 493 2 T12304 504 2 D81224 527 1 CSRT | 10000 | 00000 | 1000 | 999 | -100 | 0000 | 0000- | 100 | 2010 | 0000 | 77 | 1000 | 9 7 | 00 | 700 | 900 | 9 07 0 | 400 | 7 7 | 0 0 | 77 | ~ ~ | ~ ~ | 00 | |
| 4 4 4 4 0 . 8 . 8 . 9 . 9 . 9 . 9 . 9 . 9 . 9 . 9 | 3 4 60.1 3 3 9.5 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 33.52 | 36.9 | 36.3 | 36.3 | 335.7 | 3 3 4 4 4 4 | 34.4 | 33.8 | 333.1 33.1 32.5 5 | 32.5 | 31.8 | 31.8 | 31.2 | 30.6 | 30.6 | 30.6 | 30.6 | 30.6 | 7 29.9 7 29.9 | 29.9 | 29.9 | 7 29.9 | 29.9 | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| | Seconds hts) | | | | | | | | have a ing printed, n. | | ription | lase (EC 1.11. | 388 | 을 일 일 대 대 대 대 대 대 대 대 대 대 대 대 대 대 대 대 대 | EC 1 | 388 | 20 | | . E | (E) | C [Im | (EC 1 | (EC 1 | (E) | (EC 1 |
| version 4.5 - 2000 Compugen Ltd. | ; Search time 26.88 (without alignmen 103.668 Million c | NNVITAGPRG 29 | κί | residues parameters: 283138 | | maries | | | results predicted by chance to have to the score of the result being of the total score distribution. | SUMMARIES | Descript | catalase catalase | | | | O catalase | | | | | | | | | 2 catalase 3 catalase |
| GenCore v (c) 1993 - | 2002, 07:4 | :-09-488-737-2 7 MVNKDVKQTTAFGAPVWDDNNVITAGPRG | · 0. | .38 seqs, 96089334 satisfying chosen | 2000000000 | Match 0% Match 100% first 100 summaries | * * * | * * | _ | | Length DB ID | 505 2 C64629 505 2 F71885 | 82 2 | 96 2 | 4 63 6 | 220 | 200 | 800 | 93 2 | 83 2 92 2 | 13 2 92 2 | 92 2 | 92 | 27 1 CSHU 21 2 S6579 | 2 A5726 2 D6410 |
| Copyright protein search | ust | . 15 | | 283138 sof hits sati | length: length: | ing: Minimum Maximum Listing | PIR_71:* 1: pir1:* 2: pir2:* | 4: pirt | No. is the number of greater than or equa derived by analysis | * Query | e Match | 57 100.0 57 100.0 | 56.1 | | | | | | | | | | | | |
| OM protein - | on: | Title: Perfect score Sequence: | Scoring table | Searched: Total number | Minimum DB seq Maximum DB seq | Post-processing | Database : | | Pred. N score g and is | Result | No. Score | 1 15 | | m (| D | | | | | | | | | | |

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Caratase (Ec. 111.10) [Validated) Fibreds Mittabliss
C;Species: Proteus mirabilis
A;Variety: strain Pr. peroxide resistant
C;Species: Proteus mirabilis
A;Variety: strain Pr. peroxide resistant
C;Species: Proteus mirabilis
A;Variety: strain Pr. peroxide resistant
C;Species: Proteus mirabilis B5863
B;Buzy, A.; Bracchi, V.; Sterjiades, R.; Chroboczek, J.; Thibault, P.; Gagnon, J.; Jo
J. Protein Chem. 14, 59-72, 1995
A;Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A;Reference number: A58663 MUID:95305957
A;Accession: B58663
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S60757
R; DeShazer, D.; Wood, G.E.; Friedman, R.L.
Mol. Microbiol. 14, 132-130, 1994
A; Title: Molecular characterization of catalase from Bordetella pertussis: identifica A; Reference number: S60757; MUID: 95131725
A; Accession: S60757
A; Molecular preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-482 <DSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: Chromoprotein; heme; homotetramer; iron; metalloprotein; NADP; oxidoreduc F;53/Wodified site: methionine sulfone (Met) #status experimental F;54/93,127/Active site: His, Ser, Asn #status predicted F;33/Asinding site: heme iron (Tyr) (axial ligand) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Description: catalyzes the conversion of two of molecules of hydrogen peroxide to A, Note: this enzyme has a tightly bound NADPH cofactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475 A;Note: native Fe(III) with NADPH R;Gouet, P.; Jouve, H.M.; Dideberg, O. J. Mol. Biol. 249, 933-94, 1995 A;Title: Crystal structure of Proteus mirabilis PR catalase with and without bound A;Feference number: A58664; MUID:95311317 A;Contents: annotation; X-ray crystallography, 2.2 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Gouet, P.; Jouve, H.M.; Hajdu, J.
submitted to the Brookhaven Protein Data Bank, June 1996
A;Reference number: A67901; PDB:2CAG
A;Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A;Note: compound II, dithiothreitol reduced compound I
B;Gouet, P.; Jouve, H.M.; Dideberg, O.
submitted to the Brookhaven Protein Data Bank, July 1996
A;Reference number: A67902; PDB:2CAH
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C;Species: Bordetella pertussis
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 7.1e-06;
catalase (EC 1.11.1.6) [validated] - Proteus mirabilis
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Best Local Similarity 82.6%;
Matches 19; Conservative
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S60757
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C;Accession: F71885
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
I Yoes, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomeic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71805
A;Accession: F71885
A;Accession: F71885
A;Accession: F71885
A;Molecule type: DNA
A;Residues: 1-505 caRN>
A;Coss-references: GB:AE001510; GB:AE001439; NID:g4155371; PIDN:AAD06391.1; PID:g415538
A;Constriental source: strain J99
C;Genetics:
A;Gene: katA
C;Superfiamly: catalase
C;Genetics:
C;Cerycrids: heme; iron; metalloprotein; oxidoreductase
C;Cerycrids: heme; iron; metalloprotein; exial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                               R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujil, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID:97394467
A; Reference complete genome sequence not shown; translation not shown
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-505 <TON>
A; Coss-references: GB:AE000597; GB:AE000511; NID:g2314007; PIDN:AAD07923.1; PID:g231401
C; Superfamily: catalase
C; Superfamily: catalase
C; Keywords: chromoprotein; heme; Iron; metalloprotein; oxidoreductase
C; Scyperfamily: astalase
F; 56,95,129,Active site: His, Ser, Asn #status predicted
F; 339/Binding site: heme Iron (Tyr) (axial ligand) #status predicted
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                                                                                                                                                                                                                                                 Species: Helicobacter pylori
Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 04-Mar-2000
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Pred. No. 2e-15;
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Matches 29; Conserv
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Best Local Similarity
Matches 29; Conserv
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C;Species: Hordeum vulgare (barley)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C;Accession: S62697
R;Skadsen, R.W.; Schulze-Lefert, P.; Herbst, J.M.
Plant Mol. Biol. 29, 1005-1014, 1995
A;Title: Molecular cloning, characterization and expression analysis of two catalase A;Reference number: S62696; MUID:96145511
A;Accession: S62697
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                       Gaps
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A;Cross-references: EMBL:X61626; NID:g20191; PIDN:CAA43814.1; PID:g20192 C;Genetics:
A;Gene: cat A
A;Introns: 5/3; 272/3; 472/3
C;Superfamily: catalase
C;Superfamily: catalase
C;Superfamily: catalase
F;55.104,138/Active site: His, Ser, Asn #status predicted
F;55.104,138/Active site: His, Ser, Asn #status predicted
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Pred. No. 0.00032;
                                                                                                                                                                                                                                       Score 83.5; DB 1;
Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                                                                    53.2%;
61.5%;
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Best Local Similarity 66.7%;
Matches 14; Conservative
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Best Local Similarity 61.5
Matches 16; Conservative
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C; Superfamily: catala:
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C;Species: Oryza sativa (rice
C;Species: Oryza sativa (rice
C;Date: 31-Dec-1992 #sequence_revision 02-Jun-2000 #text_change 16-Jun-2000
C;Accession: S70588; S20873; S19823
R;Higo, K.; Higo, H.
Plant Mol. Biol. 30, 505-521, 1996
A;Title: Cloning and characterization of the rice CatA catalase gene, a homologue of the A;Reference number: S70588; MUID:96189265
A;Accession: S70588; MUID:96189265
A;Accession: S70588; MUID:96189265
A;Accession: S70588; MUID:96189265
A;Accession: S70588; MUID:96189265
A;Residues: 1-491 <-HIG>
A;Cross-references: EMBL:D29966; NID:91261857; PIDN:BAA06232.1; PID:91261858
A;Mori, H.; Higo, K.; Higo, H.; Minobe, Y.; Matsui, H.; Chiba, S.
Plant Mol. Biol. 18, 973-976, 1992
A;Title: Nucleotide and derived amino acid sequence of a catalase cDNA isolated from rice
A;Reference number: S20873; MUID:92256818
A;Accession: S20873; MUID:92256818
A;Accession: S20873; MUID:92256818
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AB0148
A;Cross-references: EMBL:U07800; NID:q494943; PIDN:AAA18481.1; PID:q494944 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalase (EC 1.11.1.6) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 0.2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB0148
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                                                                                         C; Superfamily: catalase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;57,96,130/Active site: His, Ser, Asn #status predicted
F;340/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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                                                                                                                                                                                                                                       DB 2;
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A;Residues: 1-112,'Q',114-447,'AV',450-491 <MOR>
                                                                                                                                                                                                                                                                                     3; Mismatches
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                                                                                                                                                                                                                                       Score 88;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catalase (EC 1.11.1.6) catA - rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.8%;
65.5%;
                                                                                                                                                                                                                                       56.18;
85.58;
                                                                                                                                                                                                                                                                                  19; Conservative
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C;Superfamily: catalase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
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A;Molecule type: DNA
A;Residues: 1-480 <KUR>
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                                                                        A; Gene: catA
                                                Genetics:
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Matches
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oxidoreductase;

us-09-488-737-2.rpr

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Catalase (EC 1.11.1.6) - Arabidopsis thaliana
NiAlternate names: protein M4E13.140
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: 105779; S18972
Riberan, M.; Purnelle, B.; Boutry, M.; Goffeau, A.; Hoheisel, J.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, April 1998
A; Reference number: 215451
A; Accession: T05779
A; Molecule type: DNA
A; Residues: 1-492 < ABEV >
A; Molecule type: DNA
A; Residues: 1-492 < ABEV >
A; Cross-references: EMBL:AL022023
A; Experimental source: cultivar Columbia; BAC clone M4E13
R; Chevaller, C.; Yamaquenchi, J.; McCourt, P.
S; Damitted to the EMBL Data Library, January 1992
A; Description: Isolation and characterization of a catalase cDNA from Arabidopsis tha
                                                                                                                                                                                                                                 Catalase (EC 1.11.1.6) - upland cotton
Catalase (EC 1.11.1.6) - upland cotton
C;Species: Gossypium hirstuum (upland cotton)
C;Species: Gossypium hirstuum (upland cotton)
C;Accession: 510770

R;Ni, W; Turley, R,B; Trelease, R,N.
Biochim. Biophys. Acta 1049, 219-222, 1990
A;Title: Characterization of a cDNA encoding cottonseed catalase.
A;Accession: $10770
A;Residues: 10770; MUID:90304227
A;Residues: 1-492 < NNINA
A;Residues: 1-492 < NNINA
A;Residues: 1-492 < NNINA
A;Residues: 1-492 < NNINA
A;Cross references: GB:X52135; NID:918483; PIDN:CAA36380.1; PID:918484
C;Superfamily: catalase
C;Keywords: Hene: 1ron; metalloprotein; oxidoreductase
C;Keywords: Hene: 1ron; metalloprotein; oxidoreductase
C;Stybrotise: Site: His, Ser, Asn #status predicted
F;548/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A; Residues: 1-38,'L',40-108,'A',110-153,'I',155-242,'L',244-492 <CHE>
A; Cross-references: EMBL:X64271; NID:g16214; PIDN:CAA45564.1; PID:g16215
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C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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A;Introns: 5/3; 38/1; 130/3; 389/3; 419/3; 442/2; 473/3
A;Note: M4E13.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.4%; Score 76; DB 2;
61.9%; Pred. No. 0.0025;
Live 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%; Score 75; DB 2; ilarity 61.9%; Pred. No. 0.0036; Conservative 4; Mismatches 4
                                       29
                                                                         18 TTNSGAPVWNNNSSLTVGPRG 38
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Best Local Similarity 61.9
Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserva
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A;Accession: B83113
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-482 <STO>
A;Cross-references: GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG07624.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.; Hickey, M.J.; Br
A.; Larbig, K.; Lim,
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: BB3113
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb Nature 406, 959-964, 2000
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C;Species: Gossypium hirsutum (upland cotton)
C;Bate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Mar-2000
C;Accession: S10395
R;Weiting, N.; Turley, R.B.; Trelease, R.N.
submitted to the EMBL Data Library, March 1990
A; Molecule type: mRNA
A; Residues: 1-494 < SKA>
A; Cross-references: EMBL:U20778; NID:g684947; PIDN:AAA96948.1; PID:g684948
A; Note: the authors did not translate the codon for residue 76
C; Superfamily: catalase
C; Superfamily: catalase
C; Keywords: heme; iron; metalloprotein; oxidoreductase
F; 65,104,138/Active site: His, Ser, Asn #status predicted
F; 348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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A.Residues: 1-492 <WEI>
A.Cross-references: EMBL:X52135
C.Superfamily: catalase
C.Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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                                                                                                                                                                                                                                                                                                    Length 494;
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0.0012;
8;
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Pred. No. 0.0011;
2; Mismatches 8;
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                                                                                                                                                                                                                                                                                              Query Match 50.0%;
Best Local Similarity 57.7%;
Matches 15; Conservative
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1 Similarity 57.1%;
16; Conservative
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A; Accession: S10395
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C;Superfamily: catalase
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Best Local Similarity
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C: Accession: JC7672
R; Kitamura, M.; Nakanishi, T.; Kojima, S.; Kumagai, I.; Inoue, H.
J. Biochem. 129, 357-364, 2001
A; Title: Cloning and expression of the catalase gene from the anaerobic bacterium Des A; Reference number: JC7672; MUID:21125589; PMID:11226874
A; Accession: JC7672
A; Accession: Acce
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R. Mori, H.; Imaseki, H.
Plant Physiol. 102, 691-692, 1993
A. Title: CDNA for catalase from eticlated mung bean (Vigna radiata) hypocotyls.
A. Reference number: 217208; MUID:94151449
A. Reference number: 217208; MUID:94151449
A. Reference number: 110902
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Status: preliminary;
A. Molecule type: mRNA
A. Residues: 11492 ANOR>
A. Status: preliminary;
A. Molecule type: mRNA
A. Residues: 11492 ANOR>
A. Status: preliminary;
A. Molecule type: mRNA
A. Residues: 11492 ANOR>
A. Status: preliminary;
C. Punction:
C. Punction: catalyzes the conversion of two molecules of hydrogen peroxide to two C. Superfamily: catalase
C. Superfamily: catalase
C. Superfamily: catalase
C. Superfamily: Set Name at Status predicted
F: 53.104.138/Active site: His, Ser, Asn #status predicted
F: 348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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A;Experimental source: strain CC-125 wild type mt+ 137c
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C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Vigna radiata (mung bean)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 480;
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Pred. No. 0.0069;
2; Mismatches 6
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R;Kim, J.Y.; Lee, K.O.; Lee, S.H.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z16209
A;Accession: T07911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 TINSGAPVWNNNSLTVGTRG 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catalase (EC 1.11.1.6) - mung bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.5%;
65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
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Matches 13; Conserv
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A; Residues: 1-493 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                        catalase (EC 1.11.1.6) isoenzyme 1 - barley
CiSpecies: Hordeum vulgare (barley)
CiSpacession: 56266
R:Skadsen, R.W.; Schulze-Lefert, P.; Herbst, J.M.
Altile: Molecular cloning, characterization and expression analysis of two catalase isc
A.Reference number: 562696; MUID: 96145511
A.Accession: 562696
A.Status: preliminary; nucleic acid sequence not shown
A.Residues: 1-492 <SKA>
A.Residues: 1-492 <SKA>
A.Cross-references: EMBL:U20777; NID: 9684945; PIDN: AAA96947.1; PID: 9684946
A.Cross-references: EMBL:U20777; NID: 9684945; PIDN: AAA96947.1; PID: 9684946
C.Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catalase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #text_change 22-Oct-2001
C;Accession: G89908
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Cni, A.; Mizuteni-Ti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, B. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Status: preliminary
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A;Residues: 1-507 <KUR>
A;Cross-references: GB:BAQ00018; PID:g13701132; PIDN:BAB42427.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: kata
C;Superfamily: catalase
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catalase (EC 1.11.1.6) - Desulfovibrio vulgaris
C;Species: Desulfovibrio vulgaris
C;Decies: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Keywords: heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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o.0052;
o.hes 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74; DB 2;
Pred. No. 0.005;
3; Mismatches
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Pred. No.
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                                                 18 TTNSGAPVWNNNSSMTVGPRG 38
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                   29
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55.2%;
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Best Local Similarity 61.9%;
Matches 13; Conservative
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               TTAFGAPVWDDNNVITAGPRG
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Best Local Similarity 55.2
Matches 16; Conservative
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G89908
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catalase (EC 1.11.1.6) 1 - maize
Cispecies: Zea mays (maize)
Cispecies: Zea mays (maize)
Cispecies: Zea mays (maize)
Cispecies: Zea mays (maize)
Cispecies: Jean mays (maize)
Cispecies: Jean mays (maize)
Cisterial-101-1995 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
CiAccession: S48124; JA0090
Ridun, Li; Scandalios, J.G.
Plant J. 3, 527-536, 1993
A; Title: Characterization of the catalase antioxidant defense gene Catl of maize, and A; Reference number: S48124; MUID:94035156
A; Accession: 1-492 (AGNA)
A; Accession: 1-492 (AGNA)
A; Cross-references: EMBL:860135; NID:9311238; PIDN:CAA42720.1; PID:9311239
A; Note: the authors translated the codon GTC for residue 157 as Ala
A; Note: the authors translated the codon GTC for residue 157 as Ala
B; Note: the authors translated the codon GTC for residue 157 as Ala
A; Note: the authors translated the codon GTC for residue 157 as Ala
A; Note: the authors translated the codon GTC for residue 157 as Ala
A; Note: the authors translated the codon GTC for residue 157 as Ala
A; Note: the authors translated the codon GTC for residue 157
A; Note: the authors and A; Note: Acta 951, 104-116, 1988
A; Title: Characterization of catalase transcripts and their differential expression i A; Accession: JA0090
A; Accession: JA0090
A; Accession: JA0090
A; Accession: JA0090
A; Accession: JA0090
A; A; Cross-references: GB:X12538; GB:M33104; NID:922231; PIDN:CAA31056.1; PID:922232
C; Genetics:
C; Genetics:
A; Gene: catl
A; Introns: 5/3; 38/1; 130/3; 419/3; 442/2; 473/3
C; Superfamily; catalase
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A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam Ster, E.W.

A; Fitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A; Accession: AC3220
A;Description: catalyzes the conversion of two of molecules of hydrogen peroxide .
C;Superfamily: catalase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;2-483/Product: catalase, vegetative #status predicted <MAT>
F;54,93,127/Active site: His, Ser, Asm #status predicted
F;337/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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                                                                                                                                                                                                                                                                                                                                        Score 71; DB 2; Length 483;
Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                                                  45.2%; bcc. 60.9%; Pred. No. c..
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Matches 14; Conservative
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Matches
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A; Residues: 1-483 < PDDA
A; Residues: 1-483 < PDDA
A; Residues: 1-483 < PDDA
A; Cross-references: GB: M80796; NID:g142860; PIDN: AAA22402.1; PID:g142861
B; Kunst, F; Oqasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
B; Kunst, F; Oqasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; Chc
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Gallzzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, W.; Oqawa, R.; Oqiwara, A.; Oudega, B.; Rose, M.; Sada, V.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Tergetta, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Accession: C505647
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N;Alternate names: catalase 1
C;Species: Bacillus.subtilis
C;Species: Bacillus.subtilis
C;Accession: JH0532; C69647; F44519
R;Bol, D.K.; Yasbin, R.E.
R;Bol, D.K.; Yasbin, R.E.
A;Title: The isolation, cloning and identification of a vegetative catalase gene from Ba
A;Reference number: JH0532; MUID:92097949
A;Accession: JH0532.
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R;Dowds, B.C.A.
submitted to the Protein Sequence Database, February 1993
A;Reference number: A44519
A;Accession: F44519
                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-90, 'p', 92-244, 'RS', 247-356,'V', 358-404, 'GWLPCRV', 413-434,'RW', 437-481,'G'
A; Cross-references: EMBL: X13220
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes the conversion of two molecules of hydrogenperoxide to two
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C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 493;
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Pred. No. 0.01;
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A; Residues: 1-205, 'G', 207-372, 'G', 374-483 <KUN>
                                           submitted to the EMBL Data Library, May 1997
A; Reference number: 216371
A; Accession: T08127
                                                                                                                                                                    A; Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 61.99
Matches 13; Conservative
            R; Thome, H.; Happe, T.
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A;Gene: katA
C;Function:
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C;Function:
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catalase (EC 1.11.1.6) 3 - curled-leaved tobacco c; Species: Nicotiana plumbaginifolia (curled-leaved tobacco) C; Species: Nicotiana plumbaginifolia (curled-leaved tobacco) C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C; Accession: T16969 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C; Accession: T16969 #sequence_revision Montagu, M.; Inze, D.; van Camp, W. FEBS Lett. 352, 79-83, 1994 A; Title: Molecular identification of catalases from Nicotiana plumbaginifolia (L.).
                                                                                                                                                                          Catalase (EC 1.11.1.6) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 03-Mar-2000
C;Accession: S18346; S1559
R;Isin, S.H; Allen, R.D.
Plant Mol. Biol. 17, 1263-1265, 1991
A;Title: Isolation and characterization of a pea catalase cDNA.
A;Reference number: S18346; MUID:92032793
A;Reference number: S18346
A;Reference: EMBL:X60169; NID:q20676; PIDN:CAA42736.1; PID:q20677
C;Superfamily: catalase
C;Reywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; peroxisome;
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalase (EC 1.11.1.6) - soybean
C.Species: Glycine max (soybean)
C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Mar-2000
C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Mar-2000
C.Accession: $20999
R.Allen, R.
Submitted to the EMBL Data Library, May 1992
A.Recession: $20999
A.Recession: $20999
A.Molecule type: DAL
A.Residues: 1492 ALL
A.Cross.references: EMBL:212021; NID:g18559; PIDN:CAA78056.1; PID:g18560
C.Genetics: 673: 38/1; 389/3; 419/3; 442/2; 473/3
C.Genetics: Catalase
C.Genetics: Catalase
C.Keywords: Chromoprotein; heme; iron; metalloprotein; oxidoreductase
C.Keywords: Chromoprotein; heme; iron; metalloprotein; soxidoreductase
F.55,104.138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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29
                            18 TTNSGAPVWNNNSSLTVGSRG 38
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Best Local Similarity
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Plant Mol. Biol. 25, 507-516, 1994
A;Title: Isolation and characterization of two tightly linked catalase genes from castor A;Reference number: S46297; MuID:94325474
A;Accession: S46297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catalase (EC 1.11.1.6) - upland cotton
C.Species: Gossypium hirsutum (upland cotton)
C.Species: Gossypium hirsutum (upland cotton)
C.Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C.Accession: S17493
R.Ni, W.; Trelease, R.N.
Arch. Blochem. Blophys. 289, 237-243, 1991
A.Title: Two genes encode the two subunits of cottonseed catalase.
A.Reference number: S17493; MUID:91378551
A.Molecule type: mRNA
A.Residues: 1-492 «NIW>
A.Residues: 1-492 «NIW>
C.Superfamily: catalase
C.Superfamily: catalase
C.Superfamily: Ashactive site: His, Ser, Asm #status predicted
F.504,138/Active site: His, Ser, Asm #status predicted
F.348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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                   A;Molecule type: DNA
A;Residues: 1-713 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL46177.1; PID:g17743948; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalase (EC 1.11.1.6) cat1 - castor bean
C;Species: Ricinus communis (castor bean)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S46297
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C;Superfamily: catalase
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Pred. No. 0.04;
4; Mismatches
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Pred. No. 0.043;
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Best Local Similarity 57.1%;
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
Matches 14; Conserv
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A; Residues: 1-492 <SUZ>
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A;Status: preliminary
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A Gene: GDB:CAT
A Cross-references: GDB:119049; OMIN:115500
A Cross-references: GDB:119049; OMIN:115500
A Cross-references: GDB:119049; OMIN:115500
A Introns: 22/3; 80/1; 117/1; 160/3; 195/3; 237/3; 301/3; 352/3; 399/1; 442/3; 478/3; C; Complex: homotetramer
C; Complex: homotetramer
C; Complex: homotetramer
C; Complex: homotetramer
C; Complex: blocked amino end; chromoprotein; heme; homotetramer; iron; metalloprotein; k; 2-513/Product: catalase #status experimental -kMAT>
F; 2-513/Product: catalase #status experimental -kMAT>
F; 2-513/Product: catalase, peroxisome location signal (5-[RKH]-L) motif
F; 2-513/Product: catalase, peroxisome location signal (5-[RKH]-L) motif
F; 2-514/4; AB/Active site: His, Ser, Asn #status predicted
F; 358/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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catalase (EC 1.11.1.6) - guinea pig (fragment)
c; Species: Cavia porcellus (guinea pig)
c; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Accession: S65793
R; Yuan, H.T.; Bingle, C.D.; Kelly, F.J.
Biochim. Biophys. Acta 1305, 163-171, 1996
A; Reference number: S65793
A; Title: Differential patterns of antioxidant enzyme mRNA expression in guinea pig lu A; Reference number: S65793
A; Status: prelliminary
A; Residues: 1-121 < Yuab
A; Residues: 1-121 < Yuab
A; Residues: EMBL:U39841
C; Superfamily: catalase
C; Keywords: chromoprotein; heme; iron; oxidoreductase
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CiSpecies: Bacteroil 1995
R. Rocha, E.R.; Smith, C.J.
R. Rocha, C.J.
R. R
           C; Comment: Catalase occurs in almost all aerobically respiring organisms and serves C; Genetics:
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0.022;
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Pred. No. 0.022
2; Mismatches
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61.98;
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Best Local Similarity 61.9
Matches 13; Conservative
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                                            A; Accession: T16969
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-492 (WILL)
A; Cross-references: EMBL:236977; NID:9536786; PIDN:CAA85426.1; PID:9536787
A; Experimental source: flower
A; Genetics:
A; Geneti
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R;Korneluk, R.G.; Quan, F.; Lewis, W.H.; Guise, K.S.; Willard, H.F.; Holmes, M.T.; Grave
B;Korneluk, R.G.; Quan, F.; Lewis, W.H.; Guise, K.S.; Willard, H.F.; Holmes, M.T.; Grave
B;Title: Isolation of human fibroblast catalase cDNA clones. Sequence of clones derived
A;Title: Isolation of human fibroblast catalase cDNA clones. Sequence of clones derived
A;Reference number: A00501; MUID:85034813
A;Recession: A00501
A;Molecule type: mRNA
A;Residues: 77-527 < COR>
A;Cross-references: GB:K02400; NID:g940256; PIDN:AAB59522.1; PID:g179950
A;Cross-references: fibroblast
A;Residues: 77-527 < CORS
A;Cross-references: fibroblast
A;Residues: A;Cri Hay, JG.; Lemarchand, P.; Crystal, R.G.
Clin. Invest: 93, 297-302, 1994
A;Title: Vulnerability of the human airway epithelium to hyperoxia. Constitutive express
A;Accession: 155606; MUID:94110338
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R; Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Apell, G.; Evans, L.; Bonaventura, J.; Arch. Blochem. Blophys. 214, 422-424, 1982
A; Title: The partial amino acid sequence of human erythrocyte catalase.
A; Reference number: A44717; MUID:82203126
A; Contents: annotation; sequence of peptides differing in composition from bovine
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A; Molecule type: DNA
A; Residues: 1-527 < QQDA
A; Residues: 1-527 < QQDA
A; Cross-references: GB: X04085; NID: 929682; PIDN: CAA27721.1; PID: 91228085
R; Bell, G.I.; Najarian, R.C.; Mullenbach, G.T.; Hallewell, R.A.
R; Bell, G.I.; Najarian, R.C.; Mullenbach, G.T.; Hallewell, R.A.
A; Title: CDNA sequence coding for human kidney catalase.
A; Reference number: A23651; MUID: 86286565
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Pred. No. 0.056;
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A; Reference number: S48650; MUID:95010681
A; Accession: T16969
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57.18;
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Best Local Similarity 57.1
Matches 12; Conservative
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A; Residues: 1-527 <BEL>
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A; Residues: 1-22 <RES>
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Cyaccession: S55079 R.N.; Eising, R. Blochim. Biophys. Acta 1224, 463-466, 1994 A:Treference number: S52079; MUID:95101741
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Rydchalowski, C.B.; Quigley-Landreau, F.; Bohnert, H.J.
Submitted to the EMBL Data Library, June 1998
A; Description: Different isoforms of catalase are expressed in leaves and roots of the A; Reference number: 217487
A; Accession: T12304
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL, DDBJ
C; Superfamily: catalase
C; Keywords: heme; Iron; metalloprotein; oxidoreductase
C; Keywords: heme; Iron; metalloprotein; oxidoreductase
F; 55,104,138/Active site: His, Ser, Asn #status predicted
F; 349/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                catalase (EC 1.11.1.6) - common sunflower
C;Species: Helianthus annuus (common sunflower)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
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A; Residues: 1-492 < KLES
A; Cross-references: EMBL:L28740; NID:q453528; PIDN:AAA69866.1; PID:q453529
A; Note: the authors translated the codon TTC for residue 103 as Leu
C; Superfamily: catalase
C; Superfamily: catalase
C; Stywords: heme; iron; metalloprotein; oxidoreductase
F; 55.104,138/Active site: His, Ser, Asn #status predicted
F; 55.104,138/Active site: heme iron (Tyr) (axial ligand) #status predicted
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llarity 57.1%; Pred. No. 0.16;
Conservative 4; Mismatches
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                            Mismatches
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similarity 52.4%;
11; Conservative
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-508 <TIGNS
A:Cross-references: GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22587.1; PID:g1573949; T
C:Comment: This predicted catalase is unusual in having Thr-102 replace the catalyticall
C:Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: D64103
R;FletSchmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: D64103
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                                                                                                                                                                                                                                                                                                                                                                                                                     catalase (EC 1.11.1.6) - Haemophilus influenzae (strain Rd KW20)
C;Species: Hemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 04-Mar-2000
C;Accession: D64103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catalase (EC 1.11.1.6) - wheat
C;Species: Triticum aestivum (common wheat)
C;Bate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06478
R;Saruyama, H.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                  C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;54,93,127/Active site: His, Ser, Asn #status predicted F;337/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;65,104,138/Active site: His, Ser, Asn #status predicted F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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                                                                                                                                                  Length 486;
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                                                                                                                                                                                                    9; Indels
                                                                                                                                               DB 2;
0.11;
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Pred. No. 0.12;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted to the EMBL Data Library, July 1996
A; Reference number: 215707
A; Accession: T06478
A; Molecule type: mRNA
A; Residues: 1-492 < SARA
A; Cass-references: EMBL: D86327; PIDN: BAA13068.1
A; Experimental source: seedling
                                                                                                                                                                                                 2; Mismatches
                                                                                                                                               Score 65;
Pred. No.
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                                                                                                                                                                                                                                                                               1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG 29
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61.98;
                                                                                                                                               41.4%;
55.2%;
                                                                                                                                          Query Match
Best Local Similarity 55.28
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 41.4
Best Local Similarity 61.9
Matches 13; Conservative
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C; Superfamily
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Schooles: Zea mays (maize)
C;Species: Zea mays (maize)
R;Guan, L:; Polidoros, A.N.; Scandalios, J.G.
R;Guan, L:; Polidoros, A.N.; Scandalios, J.G.
A;Reference number: S71455; MuID:96270370
A;Recorsion: S71455
A;Recorsion: S71455
A;Recorsion: S71455
A;Residues: I-492 cGUA>
A;Reference number: SRedSen, R;W.; Scandalios, J.G.
B;Reference number: S18819
A;Reference number: S18819
                             A; Residues: 399-433,'N', 438-527 <RES>
A; Cross-references: GB:K01929; NID:g203346; PIDN:AAA40885.1; PID:g203347
C; Genetics:
A; Gene: cat
A; Gene: cat
A; Introns: 22/3; 80/1; 117/1; 160/3; 195/3; 237/3; 301/3; 352/3; 399/1; 442/3; 478/3;
C; Complex: homotetramer
                                                                                                                                                                                                                                                         C) Function:
A) Description: catalyzes the conversion of two of molecules of hydrogen peroxide to C) Function:
C) Superfamily: catalase
C) Superfamily: catalase
C) Keywords: chromoprotein; heme; homotetramer; iron; metalloprotein; oxidoreductase; E;75,114,148/Active site: His, Ser, Asn #status predicted
E;358/Blinding site: heme iron (Tyr) (axial ligand) #status predicted
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-240, "RC', 244-296, 'T', 298-492 <GUW>
A; Cross-references: EMBL:X54819; NID:g22233; PIDN:CAA38588.1; PID:g22234
A; Cross-references: EMBL:X54819; NID:g22233; PIDN:CAA38588.1; PID:g22234
B; Rethands, L.A.; Skadsen, R.W.; Scandalios, J.G.
Proc. Natl: Acad. Sci. U.S.A. 87, 6927, 1990
A; Reference number: A36062; MUID:90370897
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C.Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;64,103,137/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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A;Note: the authors translated the codon AAC for residue 124 as Lys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 1;
Pred. No. 0.17;
3; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 TTGGGNPIGDKLNIMTAGPRG 48
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ilarity 57.1%;
Conservative
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Best Local Similarity
Matches 12; Conserv
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                      A; Molecule type: mRNA
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A; Residues: 1-123, 'N'
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A; Accession: A36062
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A.Residues: 1-504 <TET>
A.Cross-references: GB:AE002379; GB:AE002098; NID:g7225435; PIDN:AAF40672.1; PID:g722543
A.Cross-references: GB:AE002379; GB:AE002098; NID:g7225435; PIDN:AAF40672.1; PID:g722543
A.Staperimental source: serogroup B, strain MC58
B.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A.Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A.Accession: C81996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-504 < PAR>
A;Cross:references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83367.1; PID:g737882
A;Experimental source: serogroup A, strain 22491
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A; Residues: 1-527 cNAK>
A; Cross-references: GB:M25680; GB:M223742; NID:g203333; PIDN:AAB42378.1; PID:g203335
A; Cross-references: GB:M25680; GB:M2542, M.; Miyazawa, S.; Osumi, T.; Hashimoto, T.
Proc. Natl. Acad. Scl. U.S.A. 83, 313-317, 1986
A; Title: Complete nucleotide sequence of cDNA and deduced amino acid sequence of rat liv A; Reference number: A25965; MUID:86094381
A; Accession: A25965
                                                                                                                                                                                                                                   Ve
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: D81224; C81996
C;Accession: D81224; C81996
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salazberg, S.L.; Milte, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
A;Status: preliminary
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Nichternate names: hydrogen peroxidase; hydrogen peroxide oxidoreductase
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 03-Mar-2000
C;Accession: JU0065; A25965; I52202
G;Accession: JU0065; MUID:90006757
A;Reference number: JU0065; MUID:90006757
A;Reference number: JU0065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: katA; NMB0216; NMA0050
C;Superfamily: catalase
C;Keywords: heme; iron; metalloprotein; oxidoreductase
F;59,99,132/Active site: His, Thr, Asm #status predicted
F;342/Binding site: heme iron (Tyr) (axial ligand) #status predicted
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Biochem. Biophys. Res. Commun. 122, 831-837, 1984
A;Title: Molecular cloning of cDNA for rat liver catalase.
A;Reference number: 152202; MUID:84280086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64; DB 2;
Pred. No. 0.16;
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Best Local Similarity
Matches 12; Conserv
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1-527 <FUR>
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A; Residues: 1-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
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probable catalase (EC 1.11.1.6) [imported] - Sinorhizobium meliloti (strain 1021) mag C; Species: Sinorhizobium meliloti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C; Accession: B95843
E; Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her Proc. Natl. Acad. Sci. Us.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1,683-kb psymb megaplasmid from the N2-fixing e A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Accession: B95843
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-705 < KUR>
A; Reference number: A96039; MUID:21368234; PMID:1147104
A; Contents: annotation
A; Reference number: A96039; MUID:21368234; PMID:1147104
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01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
                       C; Accession: S49465
R; Henkle-Duehrsen, K.J.
submitted to the EMBL Data Library, October 1994
A; Reference number: S49452
A; Reference number: S49452
A; Accession: S49465
A; Molecule type: mRNA
A; Residues: 1-482 <HENA
A; Cross-references: EMBL: X82176; NID: 9558624; PIDN: CAA57666.1; PID: 9558625
C; Superfamily: catalase
C; Reywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C; S6,94,128/Active site: His, Ser, Asn *status predicted
F; 53,94, Pariding site: heme iron (Tyr) (axial ligand) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0.31;
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Pred. No. (
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61.9%; Pred. No.
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61.9%;
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Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: catC; SMb20007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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Best Local S
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C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: Dolz eb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AD3621
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    per
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                                                                                                                                                                                                              C; Species: Brucella abortus
C; Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 04-Mar-2000
C; Accession: A55227
R; Sha, Z.; Stabel, T.J.; Mayfield, J.E.
A; Bacteriol. 176, 7375-7377, 1994
A; Title: Brucella abortus catalase is a periplasmic protein lacking a standard signal a; Reference number: A55227; MUID: 95050323
A; Accession: A55227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Superfamily: catalase;Keywords: catalase;Keywords: chromoprotein; heme; homotetramer; iron; metalloprotein; oxidoreductase; ;2-499/Product: catalase #status experimental <MAT>;55,93,127/Active site: His, Ser, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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A) Status: preliminary
A; Molecule type: DNA
A; Residues: 1-507 <KUR>
A; Residues: 1-507 <KUR>
A; Cross-references: GB: AE008918; PIDN: AAL54135.1; PID:g17985098; GSPDB: GN00191
A; Experimental source: strain 16M
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:U11439; NID:9508707; PIDN:AAA64655.1; PID:9508708 C; Superfamily: catalase C; Superfamily: catalase C; Superfamily: catalase (S, Superfamer: iron; metalloprotein; oxid CS, S499/Product: catalase #status experimental <MAT> F; 5-93,127/Active site: His, Ser, Asn #status predicted F; 55,93,127/Active site: His (Str.) (axial ligand) #status predicted
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C;Species: Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
0.23;
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Pred. No. 0.23;
4; Mismatches
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Pred. No. 0.23;
4; Mismatches
                                                                                                                                                                                                        catalase (EC 1.11.1.6) - Brucella abortus
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                                      9 TTAFGAPVWDDNNVITAGPRG 29
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57.18;
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Best Local Similarity 57.1%;
Matches 12; Conservative 4
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Keywords: oxidoreductase
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A;Molecule type: DNA
A;Residues: 1-499 <SHA>
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Best Local Similarity
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C; Superfamily: cata
C; Keywords: oxidore
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A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Accession: C8662
A; Status: precliminary
A; Molecule type: DH2
A; Residues: 1.349 < CSTO>
A; Cross-references: GB:AE005176; PID:912723163; PIDN:AAK04397.1; GSPDB:GN00146
A; Experimental source: strain IL1403
A; Genetics:
A; Genetics:
A; Gene: ycj1
Query Match
Best Local Similarity 56.5%; Pred. No. 0.42;
Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;
Cy 7 KOTTAFGA--PVWDDNNVITAGP 27
Db 256 KWTTTFGARESIWDDTNVIGVTP 278
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Search completed: August 22, 2002, 07:46:14 Job time: 192 sec